



## SEQUENCE LISTING

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<120> Mu-Conopeptides

<130> 2314-242

<150> US 60/219,619  
<151> 2000-07-21

<150> US 60/245,157  
<151> 2000-11-03

<150> US 60/264,319  
<151> 2001-01-29

<150> US 60/277,270  
<151> 2001-03-21

<160> 520

<170> PatentIn version 3.0

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Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe  
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Pro Cys Cys  
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 <213> Conus arentus

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 <222> (1)..(14)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 and 12 is Pro or Hyp

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 atttcatctg atcaacatct cttctttgat ctcataaac ggtgctgcga gttgccatgc       120  
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 <213> Conus atlanticus

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      20                 25                 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe  
      35                 40                 45

Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe  
      50                 55                 60

Cys Val Pro Cys Cys  
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 <213> Conus atlanticus

<220>  
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 <222> (1)..(15)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8  
 and 13 is Pro or Hyp

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 1 5 10 15

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 <213> Conus aurisiacus

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 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttaatc agaaaagaat 180  
 gtgttgcggc gaaggccgga aatgccccag ctatttcaga aacagtcaga tttgtcattg 240  
 ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300  
 cgattgcagt 310

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 <213> Conus aurisiacus

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 1 5 10 15

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Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe  
 35 40 45

Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr  
 50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys  
 65 70

<210> 9  
 <211> 22  
 <212> PRT  
 <213> Conus aurisiacus

<220> .  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is  
 Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,  
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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Gln Ile Cys His Cys Cys  
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 <213> Conus aurisiacus

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 gacatttcat ctgagcagca tcgcttggc aatcagaaaa gaagggtgctg ccgggtggcca 180  
 tgcccccgac aaatcgacgg tgaatattgt ggctgttgcc ttggatgata accgtgttga 240  
 tgaccaactt tctcgag 257

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 <212> PRT  
 <213> Conus aurisiacus

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 20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Arg  
 35 40 45

Leu Phe Asn Gln Lys Arg Arg Cys Cys Arg Trp Pro Cys Pro Arg Gln  
 50 55 60

Ile Asp Gly Glu Tyr Cys Gly Cys Cys Leu Gly  
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 <213> Conus aurisiacus

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 <222> (1)..(19)  
 <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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 1 5 10 15

Cys Cys Leu

<210> 13  
 <211> 262  
 <212> DNA  
 <213> Conus aurisiacus

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 gacatttcat ctgagcagta tccctgttt gataagagac aaaagtgttg cactggaa 180  
 aagggttcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240  
 gttgatgacc aactttctcg ag 262

<210> 14  
 <211> 78  
 <212> PRT  
 <213> Conus aurisiacus

<400> 14  
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 1 5 10 15  
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 20 25 30  
 Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro  
 35 40 45  
 Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys  
 50 55 60  
 Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

<210> 15  
 <211> 23  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
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 <222> (1)..(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu

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 1 5 10 15  
 Lys Asn Leu Lys Cys Cys Ser  
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<210> 16  
 <211> 232  
 <212> DNA  
 <213> Conus aurisiacus

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ggcatttcac ctaaacgcca tccctggttt gatcccgta aacgggtttg caaggtgcaa 180  
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 <211> 68  
 <212> PRT  
 <213> Conus aurisiacus

<400> 17  
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 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Leu Asp  
 20 25 30

Arg His Ala Glu Arg Met His Asp Gly Ile Ser Pro Lys Arg His Pro  
 35 40 45

Trp Phe Asp Pro Val Lys Arg Cys Cys Lys Val Gln Cys Glu Ser Cys  
 50 55 60

Thr Pro Cys Cys  
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<210> 18  
 <211> 13  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp

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<210> 19  
 <211> 241  
 <212> DNA  
 <213> Conus bandus

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 gtttcatctg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcaa ctggccatgc 180  
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<210> 20  
 <211> 70  
 <212> PRT  
 <213> Conus bandus

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Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu  
 35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Trp Pro Cys Ser Met Gly Cys  
 50 55 60

Ile Pro Cys Cys Tyr Tyr  
 65 70

<210> 21

<211> .16

<212> PRT

<213> Conus bandus

<220>

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<222> (1)..(16)

<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp or  
 bromo-Trp; Xaa at residue 15 and 16 is Tyr, 125I-Tyr, mono-iodo-  
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21

Cys Cys Asn Xaa Xaa Cys Ser Met Gly Cys Ile Xaa Cys Cys Xaa Xaa  
 1 5 10 15

<210> 22

<211> 298

<212> DNA

<213> Conus betulinus

<400> 22

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agagcgtatg caggacattt catctgaaca gcatcccttg tttgatcccg tcaaaacggtg 180

ttgcgaattt ccatgccatg gatgcgtccc ttgttgctgg ccttaataac gtgtggatga 240

ccaactgtgt tatcacggcc acgtcaagtg tctaatgaat aagtaaaatg attgcagt 298

<210> 23

<211> 67

<212> PRT

<213> Conus betulinus

<400> 23

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 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ser Ser Glu Gln His Pro Leu Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys  
 50 55 60

Cys Trp Pro  
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<210> 24  
 <211> 15  
 <212> PRT  
 <213> Conus betulinus

<220>  
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 <222> (1)..(15)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

<400> 24  
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 1 5 10 15

<210> 25  
 <211> 298  
 <212> DNA  
 <213> Conus betulinus

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 ttgcgggctg ccatgcaatg gatgcgtccc ttgttgctgg ctttcataac gtgtggacga 240  
 ccaactttgt tatcacggcc acgtcaagtg tctgatgaat aagtaaaaacg attgcagt 298

<210> 26  
 <211> 68  
 <212> PRT  
 <213> Conus betulinus

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Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg His  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys  
 50 55 60

Cys Trp Pro Ser  
 65

<210> 27  
 <211> 16  
 <212> PRT  
 <213> Conus betulinus

<220>  
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 <222> (1)..(16)  
 <223> Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

<400> 27

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<210> 28  
 <211> 282  
 <212> DNA  
 <213> Conus betulinus

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 agagcgcattt cagtatgaca tggttacgtgc agtgaatccc tggtttgc cctgtcaaaag 180  
 gtgctgctcg aggaactgcg cagtatgcat cccttggta cctgaattggc cagcttgatt 240  
 atcgcggcca agagtctaat gaataagtaa aacgattgca gt 282

<210> 29  
 <211> 71  
 <212> PRT  
 <213> Conus betulinus

<400> 29  
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 1 5 10 15

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 20 25 30

Leu Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Val Asn Pro Trp Phe  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro  
 50 55 60

Cys Cys Pro Asn Trp Pro Ala  
 65 70

<210> 30  
 <211> 18  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
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 Trp or bromo-Trp

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Xaa Ala

<210> 31  
 <211> 325  
 <212> DNA  
 <213> Conus bullatus

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 tgacaggtgc tgcaaaggga agagggaatg cggcagatgg tgcagagatc actcgcgttg 240  
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 agtgaataag taaaatgatt gcagt 325

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 <211> 77  
 <212> PRT  
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 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu  
 35 40 45

Glu Lys Arg Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly  
 50 55 60

Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 33  
 <211> 23  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15  
 is Trp or bromo-Trp

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 1 5 10 15

Arg Asp His Ser Arg Cys Cys  
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<210> 34  
 <211> 326  
 <212> DNA  
 <213> Conus bullatus

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 agagcgtatg caggatgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg 120  
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 ttgcggtcga cgataacgtg ttgatgacca gctttgttat cacggctaca tcaagtgtct 240  
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tagtgattaa gtaaaacgat tgcagt 326  
 <210> 35  
 <211> 77  
 <212> PRT  
 <213> Conus bullatus

<400> 35  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Phe Ala Leu Arg Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu  
 35 40 45

Glu Lys Arg Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly  
 50 55 60

Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 36  
 <211> 23  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 15 is Trp or bromo-Trp

<400> 36  
 Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Xaa Cys  
 1 5 10 15

Arg Asp His Ser Arg Cys Cys  
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<210> 37  
 <211> 331  
 <212> DNA  
 <213> Conus bullatus

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 tgaaagggtgc tgcaaaaacg ggaagagggg gtgcggcaga tggtgccagag atcactcacg 240  
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<210> 38  
 <211> 78  
 <212> PRT  
 <213> Conus bullatus

<400> 38

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe  
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Pro Leu Leu  
 35 40 45

Glu Lys Arg Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys  
 50 55 60

Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 39  
 <211> 24  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 16 is Trp or bromo-Trp

<400> 39  
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 1 5 10 15

Cys Arg Asp His Ser Arg Cys Cys  
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<210> 40  
 <211> 337  
 <212> DNA  
 <213> Conus bullatus

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 agagcgtatg caggacgacc tttcatctga gcagcatccc ttgtttgaga agagaattgt 180  
 tgacaggtgc tgcaacaaag ggaacggaa gaggggggtgc agcagatggt gcagagatca 240  
 ctcacgttgt tgcggtcgac gatgaactgt tgatgaccga ggcttggtt atcacggcta 300  
 catcaagtgt ctagtgaata agtaaaacga ttgcagt 337

<210> 41  
 <211> 80  
 <212> PRT  
 <213> Conus bullatus

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 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe

35	40	45
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Glu Lys Arg Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg  
 50 55 60

Gly Cys Ser Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
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<210> 42  
 <211> 26  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 18 is Trp or bromo-Trp

<400> 42  
 Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser  
 1 5 10 15

Arg Xaa Cys Arg Asp His Ser Arg Cys Cys  
 20 25

<210> 43  
 <211> 337  
 <212> DNA  
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<400> 43  
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 tttatattgc tgccgaccca aacccaaacgg gcagatgtatg tgcgacagat ggtgcgaaaa 240  
 aaactcacgt tggtgcggtc gacgataatg tggtgatgac cagcttggtt atcaaggcta 300  
 catcaagtat ctatgtataa agtaaaaacga ttgcagt 337

<210> 44  
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 <212> PRT  
 <213> Conus bullatus

<400> 44  
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 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asn Pro Leu Phe Glu Lys  
 35 40 45

Ser Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp  
 50 55 60

Arg Trp Cys Glu Lys Asn Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 45  
<211> 27  
<212> PRT  
<213> Conus bullatus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 45  
Val Gly Leu Xaa Cys Cys Arg Xaa Lys Xaa Asn Gly Gln Met Met Cys  
1 5 10 15

Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys  
20 25

<210> 46  
<211> 323  
<212> DNA  
<213> Conus bullatus

<400> 46  
caagaaggat cgatagcagt tcatgatgtc taaaactggga gttttgttga ccatctgtct 60  
gcttctgttt ccccttactg ctcttccgat ggatggagat caatctgttag accgacacctc 120  
agaacgtatg caggacgacc tttcatctga gcagcatccc ttgtttgttc agaaaagaag 180  
gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg 240  
ttgttaaatg acaacgtgtc gatgaccaac ttccgtatca cgactacgccc aagtgtctaa 300  
tgaataagta aaacgattgc agt 323

<210> 47  
<211> 74  
<212> PRT  
<213> Conus bullatus

<400> 47  
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe  
35 40 45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr  
50 55 60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys  
65 70

<210> 48  
<211> 22  
<212> PRT  
<213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 48  
 Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser  
 1 5 10 15

Gln Ile Cys Ala Cys Cys  
 20

<210> 49  
 <211> 322  
 <212> DNA  
 <213> Conus bullatus

<400> 49  
 caagagggat cgatagcagt tcatgatgtc taaaactggga gtcttggta ccatctgtct 60  
 gcttcgttt ccccttttg ctcttccgca ggatggagat caacctgcag accgacctgc 120  
 tgagcgtatg caggacgaca tttcatctga gcaggatccc ttgtttgttc agaaaagaag 180  
 gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg 240  
 ttgttaaatg acaacgtgtg atgacccaact tcggtatcac gactacgcca agtgtctaat 300  
 gaataagtaa aacgattgca gt 322

<210> 50  
 <211> 74  
 <212> PRT  
 <213> Conus bullatus

<400> 50  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asp Pro Leu Phe  
 35 40 45

Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr  
 50 55 60

Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys  
 65 70

<210> 51  
 <211> 22  
 <212> PRT  
 <213> Conus bullatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 is Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at residue

ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
or O-phospho-Tyr

<400> 51  
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser  
1 5 10 15

Gln Ile Cys Ala Cys Cys  
20

<210> 52  
<211> 238  
<212> DNA  
<213> Conus capitaneus

<400> 52  
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gtttcccctt 60  
gctgctttc cactggatgg aaatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120  
gacagttcag ctgcccgtat caataacctgg attgatcatt cccattcttg ctgcagggac 180  
tgcggtaag attgtgttgg ttgttgccgg taacgtgttg atgaccaact ttctcgag 238

<210> 53  
<211> 70  
<212> PRT  
<213> Conus capitaneus

<400> 53  
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu  
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp  
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn  
35 40 45

Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp  
50 55 60

Cys Val Gly Cys Cys Arg  
65 70

<210> 54  
<211> 15  
<212> PRT  
<213> Conus capitaneus

<220>  
<221> PEPTIDE  
<222> (1)..(15)  
<223> Xaa at residue 8 is Glu or gamma-carboxy Glu

<400> 54  
Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg  
1 5 10 15

<210> 55  
<211> 323  
<212> DNA  
<213> Conus characteristicus

<400> 55  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccaaat ggatggagat caacctgcag accaacctgc 120  
 agatcgatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180  
 gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaattta tttgtggttg 240  
 ttgttaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300  
 tgaataagta aaatgattgc agt 323

<210> 56  
 <211> 74  
 <212> PRT  
 <213> Conus characteristicus

<400> 56  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
 50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

<210> 57  
 <211> 21  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty  
 r

<400> 57  
 Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe  
 1 5 10 15

Ile Cys Gly Cys Cys  
 20

<210> 58  
 <211> 316  
 <212> DNA  
 <213> Conus characteristicus

<400> 58  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120  
 cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180

ttgttgcact ccgcccgaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcgc 240  
 tggacgataa cgtgttgcgt accaacttta tcacggctac gtcaagtgtt tagtgaataa 300  
 gtaaaatgtat tgca 316  
 <210> 59  
 <211> 75  
 <212> PRT  
 <213> Conus characteristicus  
 <400> 59  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro  
 20 25 30  
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45  
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg  
 50 55 60  
 Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg  
 65 70 75  
 <210> 60  
 <211> 22  
 <212> PRT  
 <213> Conus characteristicus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp  
 <400> 60  
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys  
 1 5 10 15  
 Xaa Gln Arg Cys Cys Ala  
 20  
 <210> 61  
 <211> 314  
 <212> DNA  
 <213> Conus characteristicus  
 <400> 61  
 caagaggat cgatagcgt tcattatgtc taaaactggga gtcttggta ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120  
 agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180  
 aagaaggtgt tgccgttatac catgccccga cagctgccac ggatcttgct gctataagt 240  
 ataacatgtt gatggccagc tttgttatca cggccacgtc aagtgtctta atgaataagt 300  
 aaaacgattt cagt 314  
 <210> 62  
 <211> 72

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;400&gt; 62

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5					10					15	

Pro	Leu	Thr	Ala	Leu	Pro	Leu	Asp	Gly	Asp	Gln	Pro	Ala	Asp	Gln	Ser
	20						25						30		

Ala	Glu	Arg	Pro	Ala	Glu	Arg	Thr	Gln	Asp	Asp	Ile	Gln	Gln	His	Pro
	35						40					45			

Leu	Tyr	Asp	Pro	Lys	Arg	Arg	Cys	Cys	Arg	Tyr	Pro	Cys	Pro	Asp	Ser
				50			55				60				

Cys	His	Gly	Ser	Cys	Cys	Tyr	Lys								
65						70									

&lt;210&gt; 63

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(18)

<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is															
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos															
pho-Tyr															

&lt;400&gt; 63

Arg	Cys	Cys	Arg	Xaa	Xaa	Cys	Xaa	Asp	Ser	Cys	His	Gly	Ser	Cys	Cys
1							5				10			15	

Xaa Lys

&lt;210&gt; 64

&lt;211&gt; 292

&lt;212&gt; DNA

&lt;213&gt; Conus characteristicus

&lt;400&gt; 64

caagagggat cgatagcagt tcatgatgtc taaaactggga gccttggta ccatctgtct 60

acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

acagcgtctg caggaccgca ttccaaactga agatcatccc ttatttgatc ccaacaaacg 180

gtgttgcgg ccgggtggcat gcaacatggg atgcaaggct tggat gaccagctt 240

gttatcgcgg tcttcatgaa gtgtcttaat gaataagtaa aatgattgca gt 292

&lt;210&gt; 65

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;400&gt; 65

Met	Met	Ser	Lys	Leu	Gly	Ala	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Phe
1				5					10				15	

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro

20

25

30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe  
 35 40 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys  
 50 55 60

Lys Pro Cys Cys Gly  
 65

<210> 66  
 <211> 15  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 66  
 Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys  
 1 5 10 15

<210> 67  
 <211> 293  
 <212> DNA  
 <213> Conus characteristicus

<400> 67  
 caagagggat cgatagcagt tcatgatgtc taaaactggga gccttggta ccatctgtct 60  
 acttctgttt tcccttaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120  
 agagcgtctg catgaccgccc ttccaactga aaatcatccc ttatatgatc ccgtcaaaacg 180  
 gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataacc 240  
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 68  
 <211> 71  
 <212> PRT  
 <213> Conus characteristicus

<400> 68  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys  
 50 55 60

Trp Pro Cys Cys Met Phe Gly  
 65 70

<210> 69  
 <211> 17

<212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 69  
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Cys Met  
 1 5 10 15

Phe

<210> 70  
 <211> 232  
 <212> DNA  
 <213> Conus characteristicus

<400> 70  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taagcaggac 120  
 gtttcatctg aacagcatcc cttcttgat cccgtcaaac ggtgttgcgg ccgggtttac 180  
 atgggatgca tcccttggtt cttaaacgt gttgatgacc aactttctcg ag 232

<210> 71  
 <211> 68  
 <212> PRT  
 <213> Conus characteristicus

<400> 71  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Arg Pro Ala Glu Arg Lys Gln Asp Val Ser Ser Glu Gln His Pro Phe  
 35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Arg Arg Cys Tyr Met Gly Cys Ile  
 50 55 60

Pro Cys Cys Phe  
65

<210> 72  
 <211> 14  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 72

Cys Cys Arg Arg Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
 1 5 10

<210> 73

<211> 323

<212> DNA

<213> Conus circumcisus

<400> 73

caagaaggat cgatagcagt tcatgatgtc taaaactgggg gtattgttga ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120  
 agatcgatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacgaaa 180  
 gtgttgcggc aaagacgggc catgccccaa atatttcaaa gacaatttta ttgtgtgttg 240  
 ttgttaaatg acaacgtgtc gatgaccaac ttcgttatca cgattcgcca agtgtcttaa 300  
 tgaataagta aatgattgc agt 323

<210> 74

<211> 74

<212> PRT

<213> Conus circumcisus

<400> 74

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45

Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr  
 50 55 60

Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

<210> 75

<211> 23

<212> PRT

<213> Conus circumcisus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T  
 yr

<400> 75

Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 76

<211> 293

<212> DNA

<213> Conus dalli

<400> 76

caagagggat	cgatagcagt	tcatgatgtc	taaactggga	gccttggta	ccatctgtct	60
acttctgttt	tccctaactg	ctgttccgct	ggatggagat	caacatgcag	accaacctgc	120
agagcgtctg	caggaccgccc	ttccaactga	aaatcatccc	ttatatgatc	ccgtcaaacg	180
gtgttgcgat	gattcggaat	gcgactattc	ttgctggcct	tgctgtat	tatcataacc	240
tttgcgtatcg	cggcctcatc	aagtgtcaaa	tgaataagta	aatgattgc	agt	293

<210> 77

<211> 71

<212> PRT

<213> Conus dalli

<400> 77

Met	Met	Ser	Lys	Leu	Gly	Ala	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Phe
1				5				10					15	

Ser	Leu	Thr	Ala	Val	Pro	Leu	Asp	Gly	Asp	Gln	His	Ala	Asp	Gln	Pro
				20				25					30		

Ala	Glu	Arg	Leu	Gln	Asp	Arg	Leu	Pro	Thr	Glu	Asn	His	Pro	Leu	Tyr
	35				40					45					

Asp	Pro	Val	Lys	Arg	Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys
	50				55				60						

Trp	Pro	Cys	Cys	Ile	Leu	Ser								
65				70										

<210> 78

<211> 18

<212> PRT

<213> Conus dalli

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 78

Cys	Cys	Asp	Asp	Ser	Xaa	Cys	Asp	Xaa	Ser	Cys	Xaa	Xaa	Cys	Cys	Ile
1					5				10				15		

Leu Ser

<210> 79

<211> 299

<212> DNA

<213> Conus dalli

<400> 79

caagagggat	cgatagcagt	tcatgatgtc	taaactggga	gtcttggta	ccatctgtct	60
acttctgttt	cccccttactg	ctgttccact	ggatggagat	cagcctgcag	accgacacctgc	120

agagcgtatg caggacggca tttcatctga acatcatcca tttttgatt ccgtcaaaaa 180  
 gaaacaacag tggcgccgc cggtggcatg caacatggga tgcgagcctt gttgtggatg 240  
 accagtttg ttatcgccgc tcatgaagtg tcctaatgaa taagtaaaac gattgcagt 299

<210> 80  
 <211> 72  
 <212> PRT  
 <213> Conus dalli

<400> 80  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe  
 35 40 45

Asp Ser Val Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn  
 50 55 60

Met Gly Cys Glu Pro Cys Cys Gly  
 65 70

<210> 81  
 <211> 17  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Glu or  
 gamma-carboxy Glu; Xaa at residue 5, 6 and 15 is Pro or Hyp

<400> 81  
 Xaa Gln Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Xaa Xaa Cys  
 1 5 10 15

Cys

<210> 82  
 <211> 290  
 <212> DNA  
 <213> Conus dalli

<400> 82  
 caagaaggat cgatagcgt tcatgatgtc taaaactggga gtcttggta tcataatgtct 60  
 atttctgttt ccccttactg ctgttcagct caatggagat cagcctgcag accaatctgc 120  
 agagcgtatg caggacaaaa tttcatctga acatcatccc tttttgatc ccgtcaaacg 180  
 ttgttgcaac gcggggtttt gccgcttcgg atgcacgcct tgggtttgggt gaccagctt 240  
 gttatcgccgg cctcatcaag tgtctaatga ataagtaaaa tgattgcagt 290

<210> 83  
 <211> 69  
 <212> PRT  
 <213> Conus dalli

<400> 83  
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Phe Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Gln Leu Asn Gly Asp Gln Pro Ala Asp Gln Ser  
 20 25 30

Ala Glu Arg Met Gln Asp Lys Ile Ser Ser Glu His His Pro Phe Phe  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys  
 50 55 60

Thr Pro Cys Cys Trp  
 65

<210> 84  
 <211> 16  
 <212> PRT  
 <213> Conus dalli

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom o-Trp

<400> 84  
 Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa  
 1 5 10 15

<210> 85  
 <211> 288  
 <212> DNA  
 <213> Conus distans

<400> 85  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctttct 60  
 gcttctgttt ccccttactg ctgttccgct ggatggagat caacccgcag acggacttgc 120  
 agagcgcattg caggacgaca gttcagctgc actgattaga gactggcttc ttcaaaccgg 180  
 acagtgttgcgt gtgcattccat gccccatgcac gccttgctgt agatgaccag ctttgcattc 240  
 gcggctacgt caagtatcta atgaataagt aagtaaaacg attgcagt 288

<210> 86  
 <211> 67  
 <212> PRT  
 <213> Conus distans

<400> 86  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Phe Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gly Leu  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ser Ser Ala Ala Leu Ile Arg Asp Trp  
 35 40 45

Leu Leu Gln Thr Arg Gln Cys Cys Val His Pro Cys Pro Cys Thr Pro  
 50 55 60

Cys Cys Arg  
65

<210> 87  
<211> 14  
<212> PRT  
<213> Conus distans

<220>  
<221> PEPTIDE  
<222> (1)..(14)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 11 is Pro or Hyp

<400> 87  
Xaa Cys Cys Val His Xaa Cys Xaa Cys Thr Xaa Cys Cys Arg  
1 5 10

<210> 88  
<211> 303  
<212> DNA  
<213> Conus ermineus

<400> 88  
acctaagag ggatcgatcg cagttcatga tgtctaaact gggagccttg ttgaccatct 60  
gtctgcttct gtttcccatt actgctcttc tcatggatgg agatcagcct gcagaccgac 120  
ctgcagagcg tacggaggat gacatttcat ctgactacat tccctgttgc agttggccat 180  
gcccccgata ctccaaacggt aaacttgttt gttttgttg cttggatga taatgtgttg 240  
atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca 300  
gta 303

<210> 89  
<211> 67  
<212> PRT  
<213> Conus ermineus

<400> 89  
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys  
35 40 45

Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys  
50 55 60

Cys Leu Gly  
65

<210> 90  
<211> 20  
<212> PRT  
<213> Conus ermineus

<220>  
<221> PEPTIDE

&lt;222&gt; (1)...(20)

&lt;223&gt; Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 90

Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys  
1 5 10 15Phe Cys Cys Leu  
20

&lt;210&gt; 91

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Conus generalis

&lt;400&gt; 91

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180

aactttggat gccaacacctg ttgcctcacc tgataacgtg ttgatgacca actttctcga 240

g 241

&lt;210&gt; 92

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Conus generalis

&lt;400&gt; 92

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val  
1 5 10 15Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp  
20 25 30Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro  
35 40 45Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys  
50 55 60Gln Pro Cys Cys Leu Thr  
65 70

&lt;210&gt; 93

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus generalis

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)...(16)

&lt;223&gt; Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or Hyp

&lt;400&gt; 93

Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr  
1 5 10 15

<210> 94  
 <211> 241  
 <212> DNA  
 <213> Conus generalis

<400> 94  
 ggatccatga tgtctaaact gggagtcctg ttgaccatct gtctggttct gtttcccctt 60  
 actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat  
 gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 120  
 aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga 180  
 g 240  
 241

<210> 95  
 <211> 70  
 <212> PRT  
 <213> Conus generalis

<400> 95  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp  
 20 25 30  
 Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro  
 35 40 45  
 Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys  
 50 55 60  
 Gln Pro Cys Cys Val Pro  
 65 70

<210> 96  
 <211> 16  
 <212> PRT  
 <213> Conus generalis

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is  
 Pro or Hyp

<400> 96  
 Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa  
 1 5 10 15

<210> 97  
 <211> 862  
 <212> DNA  
 <213> Conus geographus

<400> 97  
 gtcgactcta gaggatccga caacaaagag tcaacccac tgccacgtca agagcgaagc 60  
 gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt 120  
 tgaccatctg tctgcttctg tttccctta ctgctttcc gatggatgga gatgaacctg 180

caaaccgacc tgcgagcgt atgcaggaca acatttcatac tgagcagtat cccttggttg 240  
 agaagagacg agattgtgc actccgccga agaaatgcaa agaccgacaa tgcaaacc 300  
 agagatgttgc cgctggacga taacgtgttgc atgaccaact ttatcacggc tacgtcaagt 360  
 gtttagtgaa taagtaaaat gattgcagtc ttgctcagat ttgctttgt gtttggct 420  
 aaagatcaat gaccaaaccg ttgtttgtat gcggattgtc atatatttct cgattccaaat 480  
 ccaacactag atgatttaat cacgatagat taatttcta tcaatgcctt gattttcgt 540  
 ctgtcatatc agtttgttt atatttattt ttgcgtcact gtctacacaa acgcatgcat 600  
 gcacgcacatgc acgcacacac gcacgcacgc tcgcacaaac atgcgcgcgc acgcacacac 660  
 acacacacac acacaaacac acacacaagg aatcacacaa ttattgacat tatttattt 720  
 ttcattgatg tatttggat tcggttgctt gtttttagaa tagtttgagg ccgtctttt 780  
 ggatttattt gaactgcttt attgtatacg agtacttcgt gcttgaaac actgctgaaa 840  
 ataaaaacaaa cactgacgta gc 862

&lt;210&gt; 98

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus geographus

&lt;400&gt; 98

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Phe
1				5				10					15	

Pro	Leu	Thr	Ala	Leu	Pro	Met	Asp	Gly	Asp	Glu	Pro	Ala	Asn	Arg	Pro
				20				25				30			

Val	Glu	Arg	Met	Gln	Asp	Asn	Ile	Ser	Ser	Glu	Gln	Tyr	Pro	Leu	Phe
			35				40				45				

Glu	Lys	Arg	Arg	Asp	Cys	Cys	Thr	Pro	Pro	Lys	Lys	Cys	Lys	Asp	Arg
			50		55					60					

Gln	Cys	Lys	Pro	Gln	Arg	Cys	Cys	Ala	Gly	Arg
			65		70			75		

&lt;210&gt; 99

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus geographus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(22)

&lt;223&gt; Xaa at residue 6, 7 and 17 is Pro or Hyp

&lt;400&gt; 99

Arg	Asp	Cys	Cys	Thr	Xaa	Xaa	Lys	Lys	Cys	Lys	Asp	Arg	Gln	Cys	Lys
1					5			10				15			

Xaa	Gln	Arg	Cys	Cys	Ala
				20	

&lt;210&gt; 100

&lt;211&gt; 860

&lt;212&gt; DNA

&lt;213&gt; Conus geographus

&lt;400&gt; 100

ggccagacga	caacaaagag	tcaacccac	tgccacgtca	agagcgaagc	gccacagcta	60
agacaagagg	gatcgatagc	agttcatgtat	gtctaaactg	ggagtcttgt	tgaccatctg	120
tctgcttctg	tttcccctta	ctgctctcc	gatggatgga	gatgaacctg	caaaccgacc	180
tgtcgagcgt	atgcaggaca	acatttcata	tgagcagttat	cccttgttt	agaagagacg	240
agattgttgc	actccgcca	ggaaatgcaa	agaccgacga	tgcaaacc	tgaaatgtt	300
cgctggacga	taacgtttt	atgaccaact	ttatcacggc	tagctcagtg	tttagtgaat	360
aagtaaaatg	attgcagtct	tgctcagatt	gctttgtgt	tttggctaa	gatcaatgac	420
caaaccgtt	tttgatg	gattgtcata	tatttctcga	ttccaatcca	acactagatg	480
attnaatcac	gatagattaa	tttctatca	atgcctt	tttcgtctg	tcatatcagt	540
tttggttata	tttattttt	cgtcactgtc	tacacaaacg	catgc	catgcacg	600
cacacacgca	cgcacgctcg	cacaaacatg	cgcgcgcacg	cacacacaca	cacacacaca	660
aacacacaca	cgaagcaatc	acacaattag	ttgacattat	ttatatttc	attgtatgtat	720
ttgttattcg	tttgctt	tttagaaatag	tttgaggccg	tcttttgg	tttatttgaa	780
ctgctttatt	gtatacgagt	acttcgtgct	ttgaaacact	gctgaaaata	aaacaaacac	840
tgacgttagca	aaaaaaaaaa					860

&lt;210&gt; 101

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus geographus

&lt;400&gt; 101

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1															
														15	

Pro	Leu	Thr	Ala	Leu	Pro	Met	Asp	Gly	Asp	Glu	Pro	Ala	Asn	Arg	Pro
20															
														30	

Val	Glu	Arg	Met	Gln	Asp	Asn	Ile	Ser	Ser	Glu	Gln	Tyr	Pro	Leu	Phe
35															
														45	

Glu	Lys	Arg	Arg	Asp	Cys	Cys	Thr	Pro	Pro	Arg	Lys	Cys	Lys	Asp	Arg
50															
														60	

Arg	Cys	Lys	Pro	Met	Lys	Cys	Cys	Ala	Gly	Arg	
65											
										75	

&lt;210&gt; 102

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus geographus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)...(22)

&lt;223&gt; Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 102  
 Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys  
 1 5 10 15

Xaa Met Lys Cys Cys Ala  
 20

<210> 103  
 <211> 22  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 103  
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys  
 1 5 10 15

Xaa Leu Lys Cys Cys Ala  
 20

<210> 104  
 <211> 321  
 <212> DNA  
 <213> Conus gloriamaris

<400> 104  
 ctcactatacg gaattcgagc tcggcacacg ggatcgatag cagttcatga tgtctaaact 60  
 gggagccttg ttgaccatct gtctacttct gtttcccta actgctgttc cgctggatgg 120  
 agatcaacat gcagaccaac ctgcagagcg tctgcatgac cgccttccaa ctgaaaatca 180  
 tcccttataat gatcccgtaa aacggtgttg cgatgattcg gaatgcgact attcttgctg 240  
 gccttgctgt atgtttggat aacctttgtt atcgcggcct cgataagtgt ctaatgaata 300  
 agtaaaacga ttgcagtagg c 321

<210> 105  
 <211> 71  
 <212> PRT  
 <213> Conus gloriamaris

<400> 105  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys  
 50 55 60

Trp Pro Cys Cys Met Phe Gly  
 65 70

<210> 106

<211> 17  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 106  
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met  
 1 5 10 15

Phe

<210> 107  
 <211> 257  
 <212> DNA  
 <213> Conus gloriamaris

<400> 107  
 gttcatgatg tctaaactgg gagtcttggat gatcatctgt ctacttctgt ttcccccattac 60  
 tgctgttcccg ctggatggag atcaacctgc agaccgatat gcagagcgta tgcaaggacga 120  
 catttcatctt gaacatcatc ccatgtttga tgccgtcaga gggtgttgcc atctgttggc 180  
 atgcccgttc ggtatgctcgc cttgttggat gtatcagct ttgttatcgc ggcctcatca 240  
 agtgactcta atgcaaa 257

<210> 108  
 <211> 69  
 <212> PRT  
 <213> Conus gloriamaris

<400> 108  
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe  
 35 40 45

Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys  
 50 55 60

Ser Pro Cys Cys Trp  
 65

<210> 109  
 <211> 17  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or brom

o-Trp

<400> 109  
 Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys  
 1 5 10 15

Xaa

<210> 110  
 <211> 471  
 <212> DNA  
 <213> Conus gloriamaris

<400> 110  
 gagacgacaa ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt 60  
 gaagaagggt ggagagaggt tcgtgatgtt gaaaatggga gtggtgctat tcatcttcct 120  
 ggtactgtt cccctggcaa cgctccagct ggatgcagat caacctgttag aacgatatgc 180  
 ggagaacaaa cagctcctca acccagatga aaggagggaa atcatattgc atgctctggg 240  
 gacgcgatgc tgttcttggg atgtgtgcga ccacccgagt tgtacttgct gcggcggtta 300  
 gcgccgaaca tccatggcgc tgtgctggc ggtttatcc aacaacgaca gcgtttgttg 360  
 atttcatgta tcattgcgcc cacgtctctt gtctaagaat gacgaacatg attgcactct 420  
 ggttcagatt tcgtgttctt ttctgacaat aaatgacaaa actccaaaaa a 471

<210> 111  
 <211> 71  
 <212> PRT  
 <213> Conus gloriamaris

<400> 111  
 Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro  
 1 5 10 15  
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala  
 20 25 30  
 Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu  
 35 40 45

His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro  
 50 55 60

Ser Cys Thr Cys Cys Gly Gly  
 65 70

<210> 112  
 <211> 16  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp

<400> 112  
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly

1	5	10	15
---	---	----	----

<210> 113  
 <211> 304  
 <212> DNA  
 <213> Conus laterculatus

<400> 113  
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tggaccat 60  
 ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccc 120  
 acctgcagag cgtatgcagg acgtttcatc tgaacagcat cccttgtatg atcccgtaa 180  
 acgggtttgc gactggccat gcagcggatg catcccttgt tgctaatagt aacaacgtgt 240  
 tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg 300  
 cagt 304

<210> 114  
 <211> 65  
 <212> PRT  
 <213> Conus laterculatus

<400> 114  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys  
 50 55 60

Cys  
 65

<210> 115  
 <211> 13  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or  
 bromo-Trp

<400> 115  
 Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys  
 1 5 10

<210> 116  
 <211> 313  
 <212> DNA  
 <213> Conus laterculatus

<400> 116  
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tggaccat 60

ctgtctgctt ctgtttcccc ttactgctct ggatggagat caacctgcag accgacttgc 120  
 agagcgtatg caggacgaca tttcatctga gcagcatccc tttgaaaaga gacgagactg 180  
 ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacggtt gttgcggagg 240  
 ataacgtgtt gatgaccaac tttgttatca cggctacgtc aagtgtctag tgaataagta 300  
 aaacgattgc agt 313  
  
 <210> 117  
 <211> 71  
 <212> PRT  
 <213> Conus laterculatus  
  
 <400> 117  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
  
 Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu  
 20 25 30  
  
 Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg  
 35 40 45  
  
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys  
 50 55 60  
  
 Pro Ala Arg Cys Cys Gly Gly  
 65 70  
  
 <210> 118  
 <211> 22  
 <212> PRT  
 <213> Conus laterculatus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)...(22)  
 <223> Xaa at residue 6, 17 and 17 is Pro or Hyp  
  
 <400> 118  
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys  
 1 5 10 15  
  
 Xaa Ala Arg Cys Cys Gly  
 20  
  
 <210> 119  
 <211> 314  
 <212> DNA  
 <213> Conus laterculatus  
  
 <400> 119  
 gggatcgata gcagttcatg atgtctaaac tggagtcctt gttgaccatc tgtctgcttc 60  
 tggatccct tactgctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc 120  
 gtatgcagga caacattca tctgagcagc atcaccttt tgaaaagaga cgaccaccat 180  
 gttgcaccta tgacggagt tgcctaaaag aatcatgcat gcgtaaagct tggatgcggat 240  
 gataacgtgt tgatgaccaa ctttgcattt acggctactc aagtgtctaa tgaataagta 300

aaatgattgc agta . . . . . 314

<210> 120  
 <211> 74  
 <212> PRT  
 <213> Conus laterculatus

<400> 120  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser  
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe  
 35 40 45

Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys  
 50 55 60

Glu Ser Cys Met Arg Lys Ala Cys Cys Gly  
 65 70

<210> 121  
 <211> 22  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 121  
 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys  
 1 5 10 15

Met Arg Lys Ala Cys Cys  
 20

<210> 122  
 <211> 314  
 <212> DNA  
 <213> Conus laterculatus

<400> 122  
 gggatcgata gcagttcatg atgtctaaac tgggagtc tt gttgaccacc tgtctgcttc 60  
 tttttccct tactgctctt ccgatggatg gagatcaact tgcacgccga cctgcagagc 120  
 gtatgcagga caacattca tctgagcagc atcccttctt tgaaaggaga cgaccaccat 180  
 gttgcaccta tgacggagt tgcctaaaag aatcatgcaa gctaaagct tggcggat 240  
 aataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta 300  
 aaatgattgc agta 314

<210> 123  
 <211> 74  
 <212> PRT  
 <213> Conus laterculatus

<400> 123  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Glu Arg Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys  
 50 55 60  
 Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly  
 65 70

<210> 124  
 <211> 22  
 <212> PRT  
 <213> Conus laterculatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 124  
 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys  
 1 5 10 15  
 Lys Arg Lys Ala Cys Cys  
 20

<210> 125  
 <211> 247  
 <212> DNA  
 <213> Conus leopardus

<400> 125  
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60  
 actgctcttc ggctgggttgg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120  
 gacattccag atggacagca tccgttaaat gataggcaga taaactgttg cccgtggcca 180  
 tgccctagta catgcccgcga tcaatgctgc cattaatgat aacgtgttga tgaccaactt 240  
 tctcgag 247

<210> 126  
 <211> 71  
 <212> PRT  
 <213> Conus leopardus

<400> 126  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu  
 20 25 30

Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro

35

40

45

Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr  
 50 55 60

Cys Arg His Gln Cys Cys His  
 65 70

&lt;210&gt; 127

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus leopardus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(19)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp

&lt;400&gt; 127

Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln  
 1 5 10 15

Cys Cys His

&lt;210&gt; 128

&lt;211&gt; 244

&lt;212&gt; DNA

&lt;213&gt; Conus lividus

&lt;400&gt; 128

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc ggctggtag agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120

gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttggcca 180

tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct 240

cgag 244

&lt;210&gt; 129

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Conus lividus

&lt;400&gt; 129

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu  
 20 25 30

Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro  
 35 40 45

Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser  
 50 55 60

Cys His Tyr Gln Cys Cys His  
 65 70

&lt;210&gt; 130

&lt;211&gt; 19

<212> PRT  
 <213> Conus lividus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 130

Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln  
 1 5 10 15

Cys Cys His

<210> 131

<211> 275

<212> DNA

<213> Conus lynceus

<400> 131

aaggatcgat agcagttcat gatgtctaaa ctgggagtc tggtgaccat ctgtctgctt 60  
 ctgtttcccc ttactgctct tccgatggat ggagatcaat ctgcagaccg acttgcagag 120  
 cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac 180  
 tgttgcacac ctccgaggaa atgcagagac cgagcctgca aacctaaccg ttgttgcgga 240  
 ggataagctg ttgatgacca actttgttat acggc 275

<210> 132

<211> 75

<212> PRT

<213> Conus lynceus

<400> 132

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu  
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45

Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp  
 50 55 60

Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly  
 65 70 75

<210> 133

<211> 23

<212> PRT

<213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 7, 8 and 18 is Pro or Hyp

&lt;400&gt; 133

Gly	Arg	Asp	Cys	Cys	Thr	Xaa	Xaa	Arg	Lys	Cys	Arg	Asp	Arg	Ala	Cys
1				5				10					15		

Lys	Xaa	Gln	Arg	Cys	Cys	Gly
				20		

&lt;210&gt; 134

&lt;211&gt; 803

&lt;212&gt; DNA

&lt;213&gt; Conus magus

&lt;400&gt; 134

caagagggt	cgatagcagt	tcatgatgtc	taaactggga	gtcttgttga	ccatctgtct	60
gcttctgttt	cccccattactg	ctcttccgat	ggatggagat	gaacctgcaa	accgacacctgt	120
cgagcgtatg	caggacaaca	tttcatctga	gcagttatccc	ttgtttgaga	agagacgaga	180
ttgttgcact	ccgcccgaaga	aatgcaaaga	ccgacaatgc	aaaccccaga	gatgttgcgc	240
tggacgataa	cgtgttgatg	accaactta	tcacggctac	gtcaagtgtt	tagtgaataa	300
gtaaaaatgat	tgcagtcttg	ctcagatttg	cttttgtgtt	ttggtctaaa	gatcaatgac	360
caaaccgttg	ttttgatgcg	gattgtcata	tatttctcga	ttccaatcca	acactagatg	420
attnaatcac	gatagattaa	ttttctatca	atgccttgat	ttttcgtctg	tcatatcagt	480
tttggttata	tttatttttt	cgtcaactgtc	tacacaaacg	catgcatgca	cgcacatgcacg	540
cacacacgc	cgcacgctcg	cacaaacatg	cgcgcgcacg	cacacacaca	cacacacaca	600
caaacacaca	cacgaagcaa	tcacacaaatt	agttgacatt	attnatttat	tcattgtatgt	660
attngttatt	cgtttgcttg	tttttagaat	agtttgaggc	cgttttttg	gattnatttg	720
aactgcttta	ttgtatacga	gtacttcgtg	cggggaaaca	ctgctgaaaa	taaaacaaac	780
actgacgtag	caaaaaaaaaa	aaa				803

&lt;210&gt; 135

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus magus

&lt;400&gt; 135

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5				10					15		

Pro	Leu	Thr	Ala	Leu	Pro	Met	Asp	Gly	Asp	Glu	Pro	Ala	Asn	Arg	Pro
				20				25				30			

Val	Glu	Arg	Met	Gln	Asp	Asn	Ile	Ser	Ser	Glu	Gln	Tyr	Pro	Leu	Phe
			35			40				45					

Glu	Lys	Arg	Arg	Asp	Cys	Cys	Thr	Pro	Pro	Lys	Lys	Cys	Lys	Asp	Arg
			50			55				60					

Gln	Cys	Lys	Pro	Gln	Arg	Cys	Cys	Ala	Gly	Arg
			65			70		75		

&lt;210&gt; 136

&lt;211&gt; 22

<212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 6 and 7 is Pro or Hyp

<400> 136  
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys  
 1 5 10 15

Xaa Gln Arg Cys Cys Ala  
 20

<210> 137  
 <211> 656  
 <212> DNA  
 <213> Conus magus

<400> 137  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacacctgc 120  
 agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tgagaaaaag 180  
 gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240  
 ttgttaaatg acaacgtgtc gatgaccaac ttcatatca cgactacgcc aagtgtctaa 300  
 tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatttg gtctaaagat 360  
 caatgaccaa accgttgttt tggtgtggat ttcatatata ttctcgagtc ctatccaaca 420  
 ctagatgatt taatcacgat agatctgatt ttttatcaa aggcttggtt ttctgtctgt 480  
 cacatcagtt ttgttatata ttaattttc gtcaactgatt acacacacgc atgaacgcac 540  
 agagtactaa cacatacaca cacacacaca cacacacaca cacacacaca 600  
 cacacacaca cacgcgcgcg cgccgcgcga tctagtagcg ccgcgacgc acacac 656

<210> 138  
 <211> 74  
 <212> PRT  
 <213> Conus magus

<400> 138  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
 50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

<210> 139  
 <211> 21  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty  
 r

<400> 139  
 Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe  
 1 5 10 15

Ile Cys Gly Cys Cys  
 20

<210> 140  
 <211> 594  
 <212> DNA  
 <213> Conus magus

<400> 140  
 caagaggat cgatacgagt tcatgatgtc taaaactggga gtcttggta ccatctgttt 60  
 gcttctgttt ccccttactg ctcttccgag ggatggagat caatctgttag accgacactgc 120  
 agagcgtatg caggacgaca tttcatctga gctgcattccc ttgtcaatca gaaaaagaat 180  
 gtgttgcggc gagagtgcgc catgccccag ctatccaga aacagtcaga tttgtcattg 240  
 ttgttaaatg acaacgtgtc gatgaccacc ttgcattatca cgactaatga taagtaaaat 300  
 gattgcagtc tcgctcagat ttgcgtttgt atttgggtct aaagatcaat gaccaaaccg 360  
 ttgtttgtat gtggattttc atatatttct cgagtcctat ccaacactag atgatttaat 420  
 cacgatagat ctgattttt tatcaaagcc ttggtttttc gtctgtcaca tcagttttgt 480  
 ttatatttaa ttttcgtca ctgattacac acacgcatga acgcacagac gtactaacac 540  
 atacacacac acacacacac acacacacac acacacacac acacacacac acac 594

<210> 141  
 <211> 74  
 <212> PRT  
 <213> Conus magus

<400> 141  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser  
 35 40 45

Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr  
 50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys

65

70

<210> 142  
 <211> 22  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 142  
 Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser  
 1 5 10 15

Gln Ile Cys His Cys Cys  
 20

<210> 143  
 <211> 501  
 <212> DNA  
 <213> Conus magus

<400> 143  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
 gttctgttt ccccttactg ctcttccaaat ggatggagat caacctgcag accaacctgc 120  
 agatcgatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa 180  
 gtgttgcggc cccggcgggtt catgccccgt atatttcaca gacaatttta ttgttgcgg 240  
 ttgttaaatg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300  
 tgaataaaata aatgattgc agtctcgctc agatttgctt ttgtatttgg tctaaagatc 360  
 aatgaccaaaa ccgttgcggat tttcatatat ttctcgattc ctatccaaca 420  
 ctagatgatt taatcacgat agatctgatt ttttatcaa tgccttaatt ttgttgcgtc 480  
 tcataatcagt ttgtttata t 501

<210> 144  
 <211> 74  
 <212> PRT  
 <213> Conus magus

<400> 144  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
 50 55 60

Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys

65

70

&lt;210&gt; 145

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus magus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P  
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 145

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Thr Asp  
1 5 10 15Asn Phe Ile Cys Gly Cys Cys  
20

&lt;210&gt; 146

&lt;211&gt; 454

&lt;212&gt; DNA

&lt;213&gt; Conus magus

&lt;400&gt; 146

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
gcttctgttt ccccttactg ctcttccaaat ggatggagat caacctgcag accaacctgc  
agatcgatcg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa 120  
gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaattta ttgttggtt 180  
ttgttaaatg acaacgtgtc gatgaccatc ttcattatca cgactacgcc aagtgtctaa 240  
tgaataaataa aaatgattgc agtctcgctc agatttgctt ttgttatttg gtctaaagat  
caatgaccaa accgttggtt tgggtggat tttcatatat ttctcgattc ctatccaaca 300  
ctagatgatt taatcacgat agatctgatt tttt 420  
454

&lt;210&gt; 147

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Conus magus

&lt;400&gt; 147

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
20 25 30Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
35 40 45Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr  
50 55 60Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys  
65 70

&lt;210&gt; 148

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus magus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P  
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 148

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp  
1 5 10 15Asn Phe Ile Cys Gly Cys Cys  
20

&lt;210&gt; 149

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus magus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(22)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is  
Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 149

Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg  
1 5 10 15Leu Ile Cys Xaa Cys Cys  
20

&lt;210&gt; 150

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(19)

&lt;223&gt; Xaa at residue 16 is Pro or Hyp

&lt;400&gt; 150

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa  
1 5 10 15

Cys Cys Asn

&lt;210&gt; 151

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Conus marmoreus

&lt;400&gt; 151

caagaaggat cgatagcagt tcatgatgtc taaaactggga gtcttggtga ccatctgtct 60

gcttctgttt cccgttactg ctcttccgat ggatggtgat caacctgcag accgacttgt 120

agagcgtatg caggacaaca tttcatctga gcagcatccc ttctttgaaa agagaagagg 180  
 aggctgtgc acacctccga ggaaatgcaa agaccgagcc tgcaaacctg cacgttgctg 240  
 cggcccagga taacgtttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300  
 gaataagtaa aacgattgca g 321  
  
 <210> 152  
 <211> 76  
 <212> PRT  
 <213> Conus marmoreus  
  
 <400> 152  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30  
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp  
 50 55 60  
 Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
 65 70 75  
  
 <210> 153  
 <211> 24  
 <212> PRT  
 <213> Conus marmoreus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 3, 8, 18 and 24 is Pro or Hyp  
  
 <400> 153  
 Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys  
 1 5 10 15  
 Lys Xaa Ala Arg Cys Cys Gly Xaa  
 20  
  
 <210> 154  
 <211> 296  
 <212> DNA  
 <213> Conus marmoreus  
  
 <400> 154  
 gagctcggtt ccccgacctc aagagggatc gatagcagtt catgatgtct aaactggaa 60  
 tcttggatc catctgtcta cttctatttc cccttactgc tggccgtg gatggagatc 120  
 aacctgcaga ccgacctgca gagcgtatgc aggacgacat ttcatctgaa catcatccct 180  
 tttttatcc cgtcaaacgg tggcaggt tatcatgcgg cttggatgc cacccttgg 240  
 gtggatgacc agctttgtta tcgcggcctc atcaagtgtc taatgaataa gtaaaa 296  
  
 <210> 155  
 <211> 68

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 155

Met Met Ser Lys Leu Gly Ile Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Phe Phe  
35 40 45Asp Pro Val Lys Arg Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His  
50 55 60

Pro Cys Cys Gly

65

&lt;210&gt; 156

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(14)

&lt;223&gt; Xaa at residue 12 is Pro or Hyp

&lt;400&gt; 156

Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Xaa Cys Cys  
1 5 10

&lt;210&gt; 157

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Conus marmoreus

&lt;400&gt; 157

ggcctacacc aagcttgcatt gcctgcaggc cgactctaga ggatccccga tcgatagcag 60

ttcatgatgt ctagactggg agtcttggc accatctgtc tacttctgtt tcccttact 120

gctgttccgc tggatggaga tcaacctgcg gaccgacctg cagagcgcct gcaggacgac 180

atttcatctg aacatcatcc ccattttgtat tccggcagag agtgttgcgg ttcgttcgca 240

tgccgctttg gatgcgtgcc ttgttgtgta tgaccagctt tgttatcacg gcctcatcga 300

gtgtctaattg aataagtaaa acgattgcag taggcggta ccgagctcga attcc 355

&lt;210&gt; 158

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 158

Met Met Ser Arg Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Leu Gln Asp Asp Ile Ser Ser Glu His His Pro His Phe

35

40

45

Asp Ser Gly Arg Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys  
 50 55 60

Val Pro Cys Cys Val  
 65

<210> 159

<211> 17

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 14 is Pro or Hyp

<400> 159

Xaa Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys  
 1 5 10 15

Val

<210> 160

<211> 295

<212> DNA

<213> Conus marmoreus

<400> 160

cgacacctaaag agggatcgat agcagttcat gatgtctaaa ctgggaggtct tgggtgaccat 60

ctgtctactt ctatttcccc ttactgctgt tccgctggat ggagaccaac ctgcagaccg 120

acctgcagag cgtatgcagg acgacatttc atctgaacgt catcctttt ttgatcgcag 180

caaacagtgt tgccatctgc cggcatgccg ctccggatgt acgccttggt gttgggtgatc 240

agctttgtta tcgcgtcctc atcaagtgtc taatgaataa gtaaaatgtat tgcag 295

<210> 161

<211> 67

<212> PRT

<213> Conus marmoreus

<400> 161

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg  
 35 40 45

Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro  
 50 55 60

Cys Cys Trp  
 65

<210> 162

<211> 19

<212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Xaa at residue 8 and 16 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp

<400> 162  
 Ser Lys Gln Cys Cys His Leu Xaa Ala Cys Arg Phe Gly Cys Thr Xaa  
 1 5 10 15

Cys Cys Xaa

<210> 163  
 <211> 235  
 <212> DNA  
 <213> Conus marmoreus

<400> 163  
 ggatccatga tgtctaaact gggagtcgg ttgaccatct gtctgcttct gttccccc 60  
 actgctcttc cgctggatgg agatcaacct gcagaccaac gtgcagagcg tacgcaggcc 120  
 gagaaggatt cttgcctga tccgagaatg ggctgttgcc cgttccatg caaaaccagt 180  
 tgcactactt tgtgttgcgg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 164  
 <211> 67  
 <212> PRT  
 <213> Conus marmoreus

<400> 164  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Gln Arg Ala Glu Arg Thr Gln Ala Glu Lys His Ser Leu Pro Asp Pro  
 35 40 45

Arg Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu  
 50 55 60

Cys Cys Gly  
 65

<210> 165  
 <211> 17  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 5 and 7 is Pro or Hyp

<400> 165  
 Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys  
 1 5 10 15

## Cys

&lt;210&gt; 166

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

&lt;223&gt; Xaa at residue 4 and 6 is Trp or bromo-Trp

&lt;400&gt; 166

Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser  
1 5 10 15

&lt;210&gt; 167

&lt;211&gt; 357

&lt;212&gt; DNA

&lt;213&gt; Conus marmoreus

&lt;400&gt; 167

gccaagcttg catgcctgca ggatgactct agaggatccc cacctaaga gggatcgata 60

gcagttcatg atgtctaaac tgggagtc ttgtgaccatc tgtctacttc tgtttgcct 120

tactgctgtt ccgctggatg gagatcaacc tgcagaccga cctgcagaac gtatgcagga 180

cgacatttca tctgaacgatc atccatgtt tgatgccgtc agagattgtt gcccgttgcc 240

ggcatgcccc ttggatgca acccttggatg tggatgacca gctttgttat cgggacactca 300

tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc 357

&lt;210&gt; 168

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 168

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala  
35 40 45Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro  
50 55 60Cys Cys Gly  
65

&lt;210&gt; 169

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

&lt;223&gt; Xaa at residue 4, 6, 9 and 14 is Pro or Hyp

<400> 169  
 Asp Cys Cys Xaa Leu Xaa Ala Cys Xaa Phe Gly Cys Asn Xaa Cys Cys  
 1 5 10 15

<210> 170  
 <211> 16  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 170  
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg  
 1 5 10 15

<210> 171  
 <211> 16  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 171

Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg  
 1 5 10 15  
 <210> 172  
 <211> 16  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 172  
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg  
 1 5 10 15

<210> 173  
 <211> 17  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 14 is Pro or Hyp

<400> 173  
 Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys  
 1 5 10 15

Val

<210> 174

<211> 244  
 <212> DNA  
 <213> Conus nobilis

<400> 174  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60  
 actgctttc cgctggatga agatcaacccgtacaccgac ctgcagagcg tatgcaggac 120  
 atttcatctg atcaacatct cttcttgat ctcataaac ggtgctgcga gttgccatgc 180  
 gggccagggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240  
 cgag

<210> 175  
 <211> 69  
 <212> PRT  
 <213> Conus nobilis

<400> 175  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His  
 20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe  
 35 40 45

Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe  
 50 55 60

Cys Val Pro Cys Cys  
 65

<210> 176  
 <211> 15  
 <212> PRT  
 <213> Conus nobilis

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8  
 and 13 is Pro or Hyp

<400> 176  
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys  
 1 5 10 15

<210> 177  
 <211> 262  
 <212> DNA  
 <213> Conus nobilis

<400> 177  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60  
 actgctttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120  
 gacatttcat ctgagcagta tcccttggat gataagagac aaaagtgttg cactggaaag 180  
 aaggggatcat gctccggcaa agcatgcaaa aatctcaaat gttgctctgg acgataacgt 240

gttcatgacc aactttctcg ag 262

<210> 178  
 <211> 78  
 <212> PRT  
 <213> Conus nobilis

<400> 178  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro  
 35 40 45

Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys  
 50 55 60

Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

<210> 179  
 <211> 23  
 <212> PRT  
 <213> Conus nobilis

<220>  
 <221> PEPTIDE  
 <222> (1)...(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 179  
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
 20

<210> 180  
 <211> 238  
 <212> DNA  
 <213> Conus pulicarius

<400> 180  
 ggatccatga tgtctaaact gggagtttg ttgaccatct gtctgcttct gttccccc 60  
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttcttgat cccgtcaaac ggtgttgcaa cagctgttac 180  
 atgggatgca tcccttggc cttcttagtaa taacgtgttgc atgaccaact ttctcgag 238

<210> 181  
 <211> 68  
 <212> PRT  
 <213> Conus pulicarius

<400> 181  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp

20

25

30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe  
 35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile  
 50 55 60

Pro Cys Cys Phe  
 65

<210> 182  
 <211> 14  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 182  
 Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
 1 5 10

<210> 183  
 <211> 238  
 <212> DNA  
 <213> Conus querceanus

<400> 183  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 acagctcttc agctggatgg agatcaacct gcagaccgac ctgcagagcg tacgcaggac 120  
 attgcatctg aacagtatcg aaagtttgat cagagacaga ggtgttgcca gtggccatgc 180  
 cccggtagtt gcagatgctg ccgtactggtaaacgtgttg atgaccaact ttctcgag 238

<210> 184  
 <211> 70  
 <212> PRT  
 <213> Conus querceanus

<400> 184  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys  
 35 40 45

Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys  
 50 55 60

Arg Cys Cys Arg Thr Gly  
 65 70

<210> 185  
 <211> 17  
 <212> PRT

<213> Conus quercinus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pro or Hyp; Xaa at residue 6 is Trp or bromo-Trp

<400> 185

Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg  
1 5 10 15

Thr

<210> 186

<211> 15

<212> PRT

<213> Conus quercinus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 186

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn  
1 5 10 15

<210> 187

<211> 15

<212> PRT

<213> Conus quercinus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp

<400> 187

Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn  
1 5 10 15

<210> 188

<211> 323

<212> DNA

<213> Conus radiatus

<400> 188

tcaagaagga tcgatagcag ttcatgatgt ctaaactggg agtcttggc accatctgtc 60

tgcttctgtt tccccttact gctcttccga tggatggaga tcaacctgta gaccgacttg 120

cagagcgtat gcaggacaac atttcatctg agcagcatac cttctttgaa aagagactac 180

catcgtgtt ctccttaac ttgcggctt gcccagtacc agcatgaaa cgttaaccctt 240

gttgcacagg ataacgtgtt gatgaccaac tttgttatca cggctacgtc aagtgtctag 300

tgaataagta aaacgattgc agt 323

<210> 189

<211> 76

<212> PRT

<213> Conus radiatus

<400> 189

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5				10						15	

Pro	Leu	Thr	Ala	Leu	Pro	Met	Asp	Gly	Asp	Gln	Pro	Val	Asp	Arg	Leu
				20				25					30		

Ala	Glu	Arg	Met	Gln	Asp	Asn	Ile	Ser	Ser	Glu	Gln	His	Thr	Phe	Phe
				35			40				45				

Glu	Lys	Arg	Leu	Pro	Ser	Cys	Cys	Ser	Leu	Asn	Leu	Arg	Leu	Cys	Pro
				50			55			60					

Val	Pro	Ala	Cys	Lys	Arg	Asn	Pro	Cys	Cys	Thr	Gly			
				65			70			75				

<210> 190

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp

<400> 190

Leu	Xaa	Ser	Cys	Cys	Ser	Leu	Asn	Leu	Arg	Leu	Cys	Xaa	Val	Xaa	Ala
1				5				10					15		

Cys	Lys	Arg	Asn	Xaa	Cys	Cys	Thr
				20			

<210> 191

<211> 336

<212> DNA

<213> Conus radiatus

<400> 191

agg	tgc	act	c	ta	g	g	at	g	at	g	t	c	a	t	g	g	g	60
tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	

tt	120																	
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

tt	180																	
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

tt	240																	
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

tt	300																	
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

tt	336																	
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

<210> 192

<211> 75

<212> PRT

<213> Conus radiatus

<400> 192

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5				10					15		

Pro	Leu	Thr	Ala	Leu	Pro	Met	Asp	Gly	Asp	Gln	Pro	Ala	Asp	Arg	Leu
				20			25					30			

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45

Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val  
 50 55 60

Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser  
 65 70 75

<210> 193

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20  
 is Pro or Hyp

<400> 193

Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys  
 1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser  
 20

<210> 194

<211> 326

<212> DNA

<213> Conus radiatus

<400> 194

acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct 60

gtctgcttct gtttcccggtt actgctcttc cgatggatgg tcatcaacct gcagaccgac 120

ttgttagagcg tatgcaggac aacatttcat ctgagcagca tcccttcttt gaaaagagaa 180

gaggaggctg ttgcacaccc ccgagggaaat gcaaagaccg agcctgcaaa cctgcacgtt 240

gctgcggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc 300

tagtgaataa gtaaaacgt tgca 326

<210> 195

<211> 76

<212> PRT

<213> Conus radiatus

<400> 195

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp  
 50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly

65

70

75

<210> 196  
 <211> 24  
 <212> PRT  
 <213> Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 196  
 Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys  
 1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa  
 20

<210> 197  
 <211> 238  
 <212> DNA  
 <213> Conus rattus

<400> 197  
 ggatccatga tgtctaaact gggagtcctt gtgaccatct gcctgcttct gttccctctt 60  
 gctgctttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120  
 gacagttcag ctgcctgat caatgcctgg cttgatgaat cccagacttg ctgcagtaac 180  
 tgcggtaag attgtgatgg ttgttgccag taacgtgttg atgaccaact ttctcgag 238

<210> 198  
 <211> 70  
 <212> PRT  
 <213> Conus rattus.

<400> 198  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn  
 35 40 45

Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp  
 50 55 60

Cys Asp Gly Cys Cys Gln  
 65 70

<210> 199  
 <211> 16  
 <212> PRT  
 <213> Conus rattus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or gamma-carboxy Glu

<400> 199  
 Xaa Thr Cys Cys Ser Asn Cys Gly Xaa Asp Cys Asp Gly Cys Cys Gln  
 1 5 10 15

<210> 200  
 <211> 327  
 <212> DNA  
 <213> Conus stercusmuscarum

<400> 200  
 gacctcaaga gggatcgata gcagttcgta atgtctaaac tgggagtctt gttgaccatc 60  
 tgtctgcttc tgtttcctct tactgctctt ccgatggatg gagatcaacc tgcagaccaa 120  
 cctgcagatc gtatgcagga cgacattca tctgagcagt atcccttggt tgataagaga 180  
 caaaaagtgtt gcactggaa gaaggggtca tgctccggca aagcatgcaa aaatctcaaa 240  
 tgttgctctg gacgataacg tgttgatgac caactttgtt atcacggcta cgtcaagtgt 300  
 ctaatgaata agtaaaaacga ttgcagt 327

<210> 201  
 <211> 75  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 201  
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
 1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala  
 20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp  
 35 40 45

Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys  
 50 55 60

Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

<210> 202  
 <211> 23  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)...(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 202  
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
 20

<210> 203  
 <211> 316  
 <212> DNA  
 <213> Conus stercusmuscarum

<400> 203  
 gatcgatagc agttcgtgat gtctaaactg ggagtcttgt tgaccatctg tctgcttctg 60  
 tttccccccta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt 120  
 atgcagaacg acatttcatc tgagcagtt cccttgtttg ataagagaca aaagtgttc 180  
 ggccccggcg cgtcatgccc cagatattc aaagacaatt ttatggatgg ttgtgtttaa 240  
 atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaagtgtc taatgaataa 300  
 gtaaaacgat tgcagt 316

<210> 204  
 <211> 73  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 204  
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
 1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala  
 20 25 30

Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp  
 35 40 45

Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe  
 50 55 60

Lys Asp Asn Phe Ile Cys Gly Cys Cys  
 65 70

<210> 205  
 <211> 23  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P  
 ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 205  
 Xaa Lys Cys Cys Gly Xaa Gly Ala Ser Cys Xaa Arg Xaa Phe Lys Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 206  
 <211> 331  
 <212> DNA  
 <213> Conus striatus

<400> 206  
 cgacctttca agagggatcg atagcagttc gcgtatgtcta aactgggggt attgttgacc 60  
 atctgtctgc ttctgtttcc ctttactgct cttccgatgg atgaagatca acctgcagac 120  
 caacttgaag atcgtatgca ggacgacatt tcacatgtgac agtacccctc gtttggtagg 180

agacaaaagt gttgcggcga aggctcgta tgcccaaatt atttcaaaaa caattttatt 240  
 tgtggttgtt gttaaatgac aacgtgtcga tgaccaactt cgttatcacg actacgcca 300  
 gttgtcttgc taatgataat aaaatgattc c 331  
  
 <210> 207  
 <211> 73  
 <212> PRT  
 <213> Conus striatus  
  
 <400> 207  
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
 1 5 10 15  
  
 Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu  
 20 25 30  
  
 Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val  
 35 40 45  
  
 Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe  
 50 55 60  
  
 Lys Asn Asn Phe Ile Cys Gly Cys Cys  
 65 70  
  
 <210> 208  
 <211> 23  
 <212> PRT  
 <213> Conus striatus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr  
  
 <400> 208  
 Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn  
 1 5 10 15  
  
 Asn Phe Ile Cys Gly Cys Cys  
 20  
  
 <210> 209  
 <211> 256  
 <212> DNA  
 <213> Conus striatus  
  
 <400> 209  
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttccctt 60  
 actgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 gacatttcat ctgacgagca tcccttggtt gataagagac aaaactgttg caatggggga 180  
 tgctccagca aatggtgcag agatcacgca cgttggcgtc gtcgatgata acgtgttgat 240  
 gaccaacttt ctcgag 256  
  
 <210> 210

<211> 75  
 <212> PRT  
 <213> Conus striatus

<400> 210  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asp Glu His Pro  
 35 40 45

Leu Phe Asp Lys Arg Gln Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys  
 50 55 60

Trp Cys Arg Asp His Ala Arg Cys Cys Gly Arg  
 65 70 75

<210> 211  
 <211> 20  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(20)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Trp or  
 bromo-Trp

<400> 211  
 Xaa Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Xaa Cys Arg Asp His  
 1 5 10 15

Ala Arg Cys Cys  
 20

<210> 212  
 <211> 235  
 <212> DNA  
 <213> Conus tessulatus

<400> 212  
 ggatccatga tgtctaaact gggagtcttg ttgaccatgt gtctgcttct gtttcccctt 60  
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taggcaggac 120  
 attgcaactg acgatcatcc tttgttgat cccgtcaaac ggtgctgcca caaatgctat 180  
 atgggatgca tcccttggatg cattttagaa cgtgttgatg accaactttc tcgag 235

<210> 213  
 <211> 68  
 <212> PRT  
 <213> Conus tessulatus

<400> 213  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu  
 35 40 45

Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile  
 50 55 60

Pro Cys Cys Ile  
 65

<210> 214  
 <211> 14  
 <212> PRT  
 <213> Conus tessulatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 214  
 Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile  
 1 5 10

<210> 215  
 <211> 238  
 <212> DNA  
 <213> Conus tessulatus

<400> 215  
 gatatccatga tgtctaaact gggagtcttg ttgaccatct gtgtgcttct gtttccctt 60  
 actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacgcagaac 120  
 gagcagcatac cttgtatga tcagaaaaga aagtgttgcc ggccgccatg cgccatgagc 180  
 tgcggcatgg ctaggtgttg ctattaatga taacgtgttg atgaccaact ttctcgag 238

<210> 216  
 <211> 68  
 <212> PRT  
 <213> Conus tessulatus

<400> 216  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu  
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20 25 30

Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln  
 35 40 45

Lys Arg Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala  
 50 55 60

Arg Cys Cys Tyr  
 65

<210> 217  
 <211> 18  
 <212> PRT  
 <213> Conus tessulatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1  
       25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty  
       r

<400> 217  
 Lys Cys Cys Arg Xaa Xaa Cys Ala Met Ser Cys Gly Met Ala Arg Cys  
       1              5                 10                 15

Cys Xaa

<210> 218  
 <211> 564  
 <212> DNA  
 <213> Conus textile

<400> 218  
 gagtcaaccc actgtcacgc caagagcgga cgccacagct aaggcaagaa ggatcgata 60  
 cagttcatga tgtctaaact gggagccttg ttgaccatct gtctacttct gtttccctt 120  
 actgctgttc cgctggatgg agatcaacat gcagaccaac ctgcacagcg tctgcaggac 180  
 cgcattccaa ctgaagatca tcccttattt gatcccaaca aacgggttg cccgcccgtg 240  
 gcatgcaaca tgggatgcaa gccttgtgt ggatgaccag ctttgttatac gcggtctcat 300  
 gaagtgtcta atgaataagt aaaacgattt cagtttcgtt cagatttgct gttgtat 360  
 ggtctaaaga ttaatgacca aactgttctt ttgatccgga tttcacgta tttctcgatt 420  
 cctattcaac actagataag ttaatcacga cagatctgtat tttccatcaa tgccttgctt 480  
 tttggtctgt catataaattc ttgtttatat ttaatttctc gtcactttca acacgcacac 540  
 acacacacac acacacgcgc gcgc 564

<210> 219  
 <211> 69  
 <212> PRT  
 <213> Conus textile

<400> 219  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
       1              5                 10                 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
       20                 25                 30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe  
       35                 40                 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys  
       50                 55                 60

Lys Pro Cys Cys Gly  
       65

<210> 220  
 <211> 16  
 <212> PRT  
 <213> Conus textile

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<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<400> 220
Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys Gly
1 5 10 15

<210> 221
<211> 780
<212> DNA
<213> Conus textile

<400> 221
ggatccagac gacaaagaag agtcaaccca ctgccacgtc aagagcagag cccacagcta 60
agacaagaag gatcgatagc agttcatgtat gtttaaactg ggagtcttgt tgaccatctg
tctccttctg ttttccctta atgctgttcc gttggatgga gatcaacctg cagaccaacc 120
tgcagagcgt ctgctggacg acatttcatt tgaaaataat ccctttatg atcccgccaa
acggtgttgc aggacttgcg accttgcac accttgttgt ggatgaccag cctcatcaag 180
tgtctaacga ataagtaaag cgattgcagt ctcgttcaga tttacttttgc tattctggc 240
taaagattaa tgaccaaact cttctttga tccggatgta catatatttc tcgattccta
tccaaacgcta gataagctaa tcacgacaga tctgatttc tgtcaatgcc ttgcttttg 300
gtctctcata tcactcttgt ttatatttaa tttctcgta ctatataat atatacacac 360
acacacacac ggaattccga ttgtccagta ccgttctgg gatcgaggta ttgctgcgt 420
ggcttattct gtactctttt cttctcgct tgatagtgtat gtcttctact cccatctgt 480
ctacccctgg ctgtatctt gataggcgtg tgcccttcac tggttataaaa cccctctgtat 540
cctactctct ggacgcctcg ggggccccaaac ctccaaataa agcgacatcc aatgaaaaaa 600
780

<210> 222
<211> 66
<212> PRT
<213> Conus textile

<400> 222
Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Phe Glu Asn Asn Pro Phe Tyr
35 40 45

Asp Pro Ala Lys Arg Cys Cys Arg Thr Cys Phe Gly Cys Thr Pro Cys
50 55 60

Cys Gly
65

<210> 223
<211> 12

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<212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 10 is Pro or Hyp

<400> 223  
 Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys  
 1 5 10

<210> 224  
 <211> 456  
 <212> DNA  
 <213> Conus textile

<400> 224  
 ggaacagtca accccacagc cacgccaaga gcagacagcc acagctacgt gaagaagggt 60  
 ggagagaggt tcatgatgtt gaaaatggga gtggtgctat tcatcttct ggtactgttt 120  
 cccctggcaa cgctccagct ggatgcagat caacctgttag aacgatatgc ggagaacaaa 180  
 cagctcctca acccagatga aaggaggaa atcctattgc ctgctctgag gaagttctgc 240  
 tgtgattcga attggtgcca catttcggat tgtgagtgtct gctacggta gcgccgaaca 300  
 tccatggcac tgtgctggc ggttcatcc caacaacgac agcgttgtt gatttcatgt 360  
 atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420  
 ttcgtgttct tttctgacaa taaatgacaa acctcc 456

<210> 225  
 <211> 70  
 <212> PRT  
 <213> Conus textile

<400> 225  
 Met Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe  
 1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr  
 20 25 30

Ala Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Leu  
 35 40 45

Leu Pro Ala Leu Arg Lys Phe Cys Cys Asp Ser Asn Trp Cys His Asp  
 50 55 60

Cys Glu Cys Cys Tyr Gly  
 65 70

<210> 226  
 <211> 17  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 is

s Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 226

Phe	Cys	Cys	Asp	Ser	Asn	Xaa	Cys	His	Ile	Ser	Asp	Cys	Xaa	Cys	Cys
1					5				10				15		

Xaa

<210> 227

<211> 456

<212> DNA

<213> Conus textile

<220>

<221> misc\_feature

<222> (1)..(456)

<223> n may be any nucleotide

<400> 227

caaggaacag	tcaacccac	agccacgcca	agagcagaca	gccacagcta	cgtgaagaag	60
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ggtggagaga	ggttcgtgat	gttgaaaatg	ggagtgggtgc	tattcatctt	cctgggtactg	120
------------	------------	------------	-------------	------------	-------------	-----

tttccccctgg	caacgctcca	gctggatgca	gatcaacctg	tagaacgata	tgcggagaac	180
-------------	------------	------------	------------	------------	------------	-----

aaacagctcc	tcagcccaga	tgaaaggagg	gaaatcatat	tgcatgctct	ggggacgcga	240
------------	------------	------------	------------	------------	------------	-----

tgctgttctt	gggatgtgtg	cgaccacccg	agttgtactt	gctgcggta	gcgcgaaca	300
------------	------------	------------	------------	-----------	-----------	-----

tccatggcgc	tgtgctggc	ggtttatcc	caacaacgac	agcgttgtt	gatttcatgt	360
------------	-----------	-----------	------------	-----------	------------	-----

atcattgcgc	ccacgtctct	tgtctaagaa	tgacgaacat	gattgcactc	tggttcagat	420
------------	------------	------------	------------	------------	------------	-----

ttcgtgttct	tttctgacaa	taaatgacaa	aacncc			456
------------	------------	------------	--------	--	--	-----

<210> 228

<211> 70

<212> PRT

<213> Conus textile

<400> 228

Met	Leu	Lys	Met	Gly	Val	Val	Leu	Phe	Ile	Phe	Leu	Val	Leu	Phe	Pro
1					5				10				15		

Leu	Ala	Thr	Leu	Gln	Leu	Asp	Ala	Asp	Gln	Pro	Val	Glu	Arg	Tyr	Ala
					20			25				30			

Glu	Asn	Lys	Gln	Leu	Leu	Ser	Pro	Asp	Glu	Arg	Arg	Glu	Ile	Ile	Leu
					35			40				45			

His	Ala	Leu	Gly	Thr	Arg	Cys	Cys	Ser	Trp	Asp	Val	Cys	Asp	His	Pro
					50				55			60			

Ser	Cys	Thr	Cys	Cys	Gly										
					65										70

<210> 229

<211> 15

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo  
     -Trp

<400> 229  
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys  
 1                   5                   10                   15

<210> 230  
 <211> 235  
 <212> DNA  
 <213> Conus textile

<400> 230  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt       60  
 actgctcttc cgctggatgg agatcaaccc gcagaccaag ctgcagagcg tatgcaggcc       120  
 gagcagcatac ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt       180  
 tgcagatatt tgtgttgcgg gtgatgataa cgtgttcatg accaacttgc tcgag       235

<210> 231  
 <211> 67  
 <212> PRT  
 <213> Conus textile

<400> 231  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu  
 1                   5                   10                   15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp  
 20                   25                   30

Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln  
 35                   40                   45

Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu  
 50                   55                   60

Cys Cys Gly  
 65

<210> 232  
 <211> 16  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1  
     25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty  
     r

<400> 232  
 Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys  
 1                   5                   10                   15

<210> 233  
 <211> 321  
 <212> DNA  
 <213> Conus tulipa

<400> 233  
 cgacctcaag agggatcgat agcagttcat gtctaaactg ggagtcttgc tgacaatctg 60  
 tctgcttctg tttccctta ctgctctgcc gatggatgga gatgaacctg cagaccgacc 120  
 tgcagagcgt atgcaggaca acatttcatc tgagcagcat cccttgggg aggagagaca 180  
 cggatgtgc aaggggcccg aaggatgctc ctccagagaa tgcagacccc aacattgttg 240  
 cggtcgacga taacgtttgc agggccact ttgttatcac ggctacgtca agtgttttagt 300  
 gaataagtaa aatgattgca g 321

<210> 234  
 <211> 74  
 <212> PRT  
 <213> Conus tulipa

<400> 234  
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro  
 1 5 10 15

Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro Ala  
 20 25 30

Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe Glu  
 35 40 45

Glu Arg His Gly Cys Cys Lys Gly Pro Glu Gly Cys Ser Ser Arg Glu  
 50 55 60

Cys Arg Pro Gln His Cys Cys Gly Arg Arg  
 65 70

<210> 235  
 <211> 21  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 8 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hyp

<400> 235  
 His Gly Cys Cys Lys Gly Xaa Xaa Gly Cys Ser Ser Arg Xaa Cys Arg  
 1 5 10 15

Xaa Gln His Cys Cys  
 20

<210> 236  
 <211> 287  
 <212> DNA  
 <213> Conus figulinus

<400> 236  
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgcgtc ccatctgtct 60  
 gcttctgatt ccccttactg ctctttcgct ggatggagat caacctgcag accgacacctgc 120  
 agagcgtatg caggatggaa tttcatctga acagcatccc atgtttgatc ccgtcagacg 180

gtgttgcgg tggccatgca acataggatg cgtaccttgt tgttgatgac cagtttgtt 240  
 atcgcggcct catcaaatgt ctaatgaata agtaaaacga ttgcagt 287  
 <210> 237  
 <211> 67  
 <212> PRT  
 <213> Conus figulinus

<400> 237  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Ile 1  
 5 10 15

Pro Leu Thr Ala Leu Ser Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu Gln His Pro Met Phe  
 35 40 45

Asp Pro Val Arg Arg Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val  
 50 55 60

Pro Cys Cys  
 65

<210> 238  
 <211> 14  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 3, 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp  
 or bromo-Trp

<400> 238  
 Cys Cys Xaa Xaa Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys 1  
 5 10

<210> 239  
 <211> 283  
 <212> DNA  
 <213> Conus figulinus

<400> 239  
 caagaggat cgatagcgt tcatgatgtt taaactggga gtcctgttga ccatctgtat 60  
 gcttctgttt ccctttactg ctcttccgct ggatggagag caacctgcag accaacctgc 120  
 agagcgcattt cagtatgaca tggttacgtgc aatgaatccc tggtttgc tggcgtcaaaag 180  
 gtgctgtctcg aagaactgctcg cagtatgcattt cccttgc tggcgtcaactga ccagcttgc 240  
 tatcgcggcc aaggctctaa tgaataagta aaacgattgc agt 283

<210> 240  
 <211> 67  
 <212> PRT  
 <213> Conus figulinus

<400> 240  
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu Leu Phe 1  
 5 10 15

Pro Phe Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Met Asn Pro Trp Phe  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro  
 50 55 60

Cys Cys Pro  
 65

<210> 241  
 <211> 14  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 241  
 Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa  
 1 5 10

<210> 242  
 <211> 286  
 <212> DNA  
 <213> Conus figulinus

<400> 242  
 caagagggat cgatagcagt tcatgatgtc taaaactgaga gtcttggta ccttatgtct 60  
 gcttctgttt ccccttactg ctcttccgct gaatgaagat caacctgcag agcgtatgca 120  
 ggacgacaat tcatctgagc agcacccctt gtatgaccac aaacgaaagt gttgccggtg 180  
 gccatgcccc gcaagatgct gctcttggta cctgtaataa cgtgttggcc aactttgtta 240  
 tcacggccac gtcaaattgtt taatgaataa gtaaaacgat tgcagt 286

<210> 243  
 <211> 64  
 <212> PRT  
 <213> Conus figulinus

<400> 243  
 Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Leu Phe.  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met  
 20 25 30

Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg  
 35 40 45

Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu  
 50 55 60

<210> 244  
 <211> 15  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or  
 bromo-Trp

<400> 244  
 Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu  
 1 5 10 15

<210> 245  
 <211> 301  
 <212> DNA  
 <213> Conus figulinus

<400> 245  
 caagagggat cgatacgagt tcatgatgtc taaactggga gtcttggta ccttatgtct 60  
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caagctgcag accgacactgc 120  
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacggtg 180  
 ttgcgagttt tcacgctgcc ttggatgcgt cccttggta 240  
 tgacccaactg tgttatcacg gccacgtcaa gtgtcta 300  
 t 301

<210> 246  
 <211> 68  
 <212> PRT  
 <213> Conus figulinus

<400> 246  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro  
 50 55 60

Cys Cys Thr Ser  
 65

<210> 247  
 <211> 16  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 3 and 12 is Pro or Hyp

<400> 247  
 Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser  
 1 5 10 15

<210> 248

<211> 301  
 <212> DNA  
 <213> Conus figulinus

<400> 248  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccttatgtct 60  
 gcttcgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120  
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacggtg 180  
 ttgcgagttg tcaaaatgcc atggatgcgt cccttggta atacctaata aacgtgcgga 240  
 tgaccaactg tgttatcactg gccacgtcaa gtgtctaata aataagtaaa atgattgcag 300  
 t 301

<210> 249  
 <211> 68  
 <212> PRT  
 <213> Conus figulinus

<400> 249  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro  
 50 55 60

Cys Cys Ile Pro  
 65

<210> 250  
 <211> 16  
 <212> PRT  
 <213> Conus figulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 and 16 is Pro or Hyp

<400> 250  
 Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa  
 1 5 10 15

<210> 251  
 <211> 298  
 <212> DNA  
 <213> Conus quercinus

<400> 251  
 caagagggat cgatagcagt tcatgatgtc taaactcgga gtcttggta ccatctgtct 60  
 gggttcgttt ccccttacag ctcttcagct ggatggagat caacctgcag accgacctgc 120  
 agagcgtacg caggacattt catctgaaca gtatcgaaag tttgatcaga gacagaggtg 180

ttgccgggtgg ccatgccccg gtagttgcag atgctgccgt tatcgtaac gtgttgggtga 240  
 ccagctttgt tatacagacc acgccaagtg tctaacaat aagtaaaaatg attgcagt 298  
 <210> 252  
 <211> 68  
 <212> PRT  
 <213> Conus quercinus

<400> 252  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Thr Gln Asp Ile Ser Ser Glu Gln Tyr Arg Lys Phe Asp  
 35 40 45

Gln Arg Gln Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys  
 50 55 60

Cys Arg Tyr Arg  
 65

<210> 253  
 <211> 18  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr  
 o or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 17  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-  
 phospho-Tyr

<400> 253  
 Xaa Arg Cys Cys Arg Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg  
 1 5 10 15

Xaa Arg

<210> 254  
 <211> 313  
 <212> DNA  
 <213> Conus quercinus

<400> 254  
 caagagggtt cgatagcagt tcatgatgtc taaaactggga gtcttgggtga ccatctgtct 60  
 gcttctgttt ccccttactg ctcttccact ggatggagat caacctgcag atcaatctgc 120  
 agagcgacct gcagagcgta cgcaggacga cattcagcag catccgttat atgatccgaa 180  
 aagaaggtgt tgccgttatac catgccccga cagctgccac ggatcttgct gctataagt 240  
 ataacatgtt gatggccagc tttgttatca cggccacgtc aagtgtctaa tgaataagt 300  
 aaacgattgc agt 313

<210> 255  
 <211> 72

&lt;212&gt; PRT

&lt;213&gt; Conus quercinus

&lt;400&gt; 255

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe  
1 5 10 15Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ser  
20 25 30Ala Glu Arg Pro Ala Glu Arg Thr Gln Asp Asp Ile Gln Gln His Pro  
35 40 45Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser  
50 55 60Cys His Gly Ser Cys Cys Tyr Lys  
65 70

&lt;210&gt; 256

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Conus quercinus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(18)

<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 and 17 is  
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos  
pho-Tyr

&lt;400&gt; 256

Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys  
1 5 10 15

Xaa Lys

&lt;210&gt; 257

&lt;211&gt; 256

&lt;212&gt; DNA

&lt;213&gt; Conus wittigi

&lt;400&gt; 257

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccatt 60

actgctcttc cgggtgggtgg agatcagcct gcagaccgac ttgcagagcg tatgcaggac 120

gacacttcat ctgagcagca tccctttgaa aagagactac catcatgttg cgacttttag 180

aggcttgcg tagtaccagc atgcatacgt catcagtgtt gcacaggata acgtgtttag 240

gaccaacttt ctcgag 256

&lt;210&gt; 258

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Conus wittigi

&lt;400&gt; 258

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe  
1 5 10 15Pro Ile Thr Ala Leu Pro Val Gly Gly Asp Gln Pro Ala Asp Arg Leu  
20 25 30

Ala Glu Arg Met Gln Asp Asp Thr Ser Ser Glu Gln His Pro Phe Glu  
 35 40 45

Lys Arg Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro  
 50 55 60

Ala Cys Ile Arg His Gln Cys Cys Thr Gly  
 65 70

<210> 259  
 <211> 23  
 <212> PRT  
 <213> Conus wittigi

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 8 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 14 is Pro or Hyp

<400> 259  
 Leu Xaa Ser Cys Cys Asp Phe Xaa Arg Leu Cys Val Val Xaa Ala Cys  
 1 5 10 15

Ile Arg His Gln Cys Cys Thr  
 20

<210> 260  
 <211> 14  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

<400> 260  
 Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa  
 1 5 10

<210> 261  
 <211> 259  
 <212> DNA  
 <213> Conus tulipa

<220>  
 <221> misc\_feature  
 <222> (1)..(259)  
 <223> n may be any nucleotide

<400> 261  
 ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gttccctt 60  
 actgctctgc cgatggatgg agatgaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 aacatttcat ctgagcagca tcccttgttt gaggagagac acggatgttgc gaggggccg 180  
 aagggatgtt cctccagaga atgcagaccc caacattgtt gcggtcgacg ataacgtgtt 240  
 gatgaccaac tntctcgag 259

<210> 262

<211> 75  
 <212> PRT  
 <213> Conus tulipa

<400> 262  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Leu Phe  
 35 40 45

Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg  
 50 55 60

Glu Cys Arg Pro Gln His Cys Cys Gly Arg Arg  
 65 70 75

<210> 263  
 <211> 21  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa at residue 5 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hyp

<400> 263  
 His Gly Cys Cys Xaa Gly Xaa Lys Gly Cys Ser Ser Arg Xaa Cys Arg  
 1 5 10 15

Xaa Gln His Cys Cys  
 20

<210> 264  
 <211> 262  
 <212> DNA  
 <213> Conus aurisiacus

<220>  
 <221> misc\_feature  
 <222> (1)..(262)  
 <223> n may be any nucleotide

<400> 264  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60  
 actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120  
 gacatttcat ctgagcagta tcccttggtt gataagagac aaaagtgttg cactggagg 180  
 aaggggtcat gctccggcaa agcatgcaaa aatctcaa at gttgctctgg acgataacgt 240  
 gttgatgacc aactttctcg an 262

<210> 265  
 <211> 76  
 <212> PRT  
 <213> Conus aurisiacus

<400> 265  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe  
 35 40 45

Asp Lys Arg Gln Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly  
 50 55 60

Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg  
 65 70 75

<210> 266

<211> 23

<212> PRT

<213> Conus aurisiacus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 266

Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
 20

<210> 267

<211> 239

<212> DNA

<213> Conus betulinus

<400> 267

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

actgctgttc cggtggatgg agatcaacct gcagaccaac ctgcagagcg tatgcagaac 120

gagcagcatc cctcgttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata 180

tgcggcatgg ctaggtgttg ctgcgtcatg ataacgtgtt gatgaccaac tttctcgag 239

<210> 268

<211> 71

<212> PRT

<213> Conus betulinus

<400> 268

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg  
 35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
 50 55 60

Cys Phe Val Met Ile Thr Cys  
65 70

<210> 269  
<211> 23  
<212> PRT  
<213> Conus betulinus

<220>  
<221> PEPTIDE  
<222> (1)..(23)  
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or  
bromo-Trp

<400> 269  
Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Phe Val Met Ile Thr Cys  
20

<210> 270  
<211> 226  
<212> DNA  
<213> Conus betulinus

<220>  
<221> misc\_feature  
<222> (1)..(226)  
<223> n may be any nucleotide

<400> 270  
ggatccatga tgtctaaact gggagtcttg ttgatcatct gtctgcttct gtttcccctt 60  
actgctgttc cgctggatgg agatcagcct gcagagcgta cgcagatcga gcagcatccc 120  
ttgtttgacc agaaaagaag gtgttgccgg tggccatgcc ccagtagatg cggcatggct 180  
agggtttgct tcgtcatgat aacgtgttga tgancgacct ctcnag 226

<210> 271  
<211> 67  
<212> PRT  
<213> Conus betulinus

<400> 271  
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Glu Arg Thr  
20 25 30

Gln Ile Glu Gln His Pro Leu Phe Asp Gln Lys Arg Arg Cys Cys Arg  
35 40 45

Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys Cys Phe Val Met  
50 55 60

Ile Thr Cys  
65

<210> 272  
<211> 23  
<212> PRT

<213> Conus betulinus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or bromo-Trp

<400> 272

Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Arg Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Phe Val Met Ile Thr Cys  
20

<210> 273

<211> 262

<212> DNA

<213> Conus parius

<400> 273

ggatccatga tgtctaaact gggagtcgg ttgaccatct gtctgcttct gtttcccctt 60

actgctcttc cgatggatgg tgatcaacct gcagaccgac ttgttagagcg tatgcaggac 120

aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggaggctg ttgcacaccc 180

ccgaagaaat gcaaagaccg agcctgcaaa cctgcacggt gctgcggccc aggataacgt 240

gttcatgacc aactttctcg cc 262

<210> 274

<211> 76

<212> PRT

<213> Conus parius

<400> 274

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp  
50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
65 70 75

<210> 275

<211> 24

<212> PRT

<213> Conus parius

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 275

Arg Gly Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Ala Cys

1

5

10

15

Lys Xaa Ala Arg Cys Cys Gly Xaa  
 20

&lt;210&gt; 276

&lt;211&gt; 259

&lt;212&gt; DNA

&lt;213&gt; Conus parius

&lt;400&gt; 276

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gttcccccctt 60  
 actgctcttc cgatggatgg tgcataacct gcagaccgac ttgttagagcg tatgcaggac 120  
 aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cacacctccg 180  
 agaaaaatgca aagaccgagc ctgcaaacct gcacgttgtt gcggcccagg ataacgtgtt 240  
 gatgaccaac tttctcgag 259

&lt;210&gt; 277

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus parius

&lt;400&gt; 277

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45

Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg  
 50 55 60

Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
 65 70 75

&lt;210&gt; 278

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus parius

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

&lt;223&gt; Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

&lt;400&gt; 278

Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys  
 1 5 10 15

Xaa Ala Arg Cys Cys Gly Xaa  
 20

&lt;210&gt; 279

&lt;211&gt; 241

&lt;212&gt; DNA

&lt;213&gt; Conus coronatus

<400> 279  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60  
 actgccccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgctgcga ttggccatgc 180  
 atcccaggat gcaccccttg ttgcttgct tgataacgtg ttgatgacca actttctcga 240  
 g 241

<210> 280  
 <211> 68  
 <212> PRT  
 <213> Conus coronatus

<400> 280  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro  
 50 55 60

Cys Cys Leu Pro  
 65

<210> 281  
 <211> 16  
 <212> PRT  
 <213> Conus coronatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 5, 8, 12 and 16 is Pro or Hyp; Xaa at residue 4 is  
 Trp or bromo-Trp

<400> 281  
 Cys Cys Asp Xaa Xaa Cys Ile Xaa Gly Cys Thr Xaa Cys Cys Leu Xaa  
 1 5 10 15

<210> 282  
 <211> 244  
 <212> DNA  
 <213> Conus musicus

<400> 282  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccttt 60  
 tctgctttc cgatggatga agatcaactt gcagacctac ctgcagagcg tatgcgggac 120  
 actgcaactg tagatcatcc ctcctatgat cctgacaaag cgtgctgcga gcagagctgt 180  
 acaaactatgct ttccgtgctg ctagccttga acacagtaac gtgttgatga ccaactttct 240  
 cgag 244

<210> 283

<211> 65  
 <212> PRT  
 <213> Conus musicus

<400> 283  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Ser Ala Leu Pro Met Asp Glu Asp Gln Leu Ala Asp Leu Pro  
 20 25 30

Ala Glu Arg Met Arg Asp Thr Ala Thr Val Asp His Pro Ser Tyr Asp  
 35 40 45

Pro Asp Lys Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys  
 50 55 60

Cys  
 65

<210> 284  
 <211> 14  
 <212> PRT  
 <213> Conus musicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue4 is Glu or gamma-carboxy Glu; Xaa at residue 12 is Pro or Hyp

<400> 284  
 Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Phe Xaa Cys Cys  
 1 5 10

<210> 285  
 <211> 14  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 4 is Glu or gamma-carboxy Glu; Xaa at residue 12 is Pro or Hyp

<400> 285  
 Ala Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys  
 1 5 10

<210> 286  
 <211> 14  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

<400> 286  
 Cys Cys Xaa Gln Ser Cys Thr Thr Cys Met Xaa Cys Cys Xaa  
 1 5 10

<210> 287  
 <211> 235  
 <212> DNA  
 <213> Conus pennaceus

<400> 287  
 ggatccatga tgtctaaact gggagtcctg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctcttc cgctggatgg agatcaacct gcataccaag ctgcagagcg tatgcaggcc 120  
 gagcatcatc ccttgtttga tcagaaaaga cggtgctgca agttccatg ccccgatagt 180  
 tgcaaataatt tgtgttgcgg gtgatgataa catgttgatg accaacttcc tttag 235

<210> 288  
 <211> 65  
 <212> PRT  
 <213> Conus pennaceus

<400> 288  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Tyr Gln Ala  
 20 25 30

Ala Glu Arg Met Gln Ala Glu His His Pro Leu Phe Asp Gln Lys Arg  
 35 40 45

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys  
 50 55 60

Gly  
 65

<210> 289  
 <211> 16  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty  
 r

<400> 289  
 Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Lys Xaa Leu Cys Cys  
 1 5 10 15

<210> 290  
 <211> 241  
 <212> DNA  
 <213> Conus pulicarius

<400> 290  
 ggatccatga tgtctaaact gggagtcctg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctcttc cgatggatgg tgatcaactt gcagaccgac ttgttagagcg tatgcaggac 120  
 aacatttcat ctgagcagca tcccttctt gatccgtca aacggtgttgcgtcagctgt 180  
 tacatggat gcatcccttg ttgcttcttag taataacgtt ttgatgacca actttctcga 240

g

241

<210> 291  
 <211> 67  
 <212> PRT  
 <213> Conus pulicarius

<400> 291  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Asp Arg Leu  
 20 25 30  
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45  
 Asp Pro Val Lys Arg Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro  
 50 55 60

Cys Cys Phe  
 65

<210> 292  
 <211> 14  
 <212> PRT  
 <213> Conus pulicarius

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 292  
 Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
 1 5 10

<210> 293  
 <211> 244  
 <212> DNA  
 <213> Conus pulicarius

<400> 293  
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtgtccctt 60  
 actgctttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat  
 gacacttcag ctgcacagat tttcggttt gatccgtca aacggtgctg caaattgcta 120  
 tgctactcg gatgcactcc ttgttgccat atttgataac gtgttgatga ccaactttct  
 180  
 cgag 244

<210> 294  
 <211> 67  
 <212> PRT  
 <213> Conus pulicarius

<400> 294  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Cys  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro

20

25

30

Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys  
 50 55 60

Cys His Ile  
 65

&lt;210&gt; 295

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus pulicarius

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

<223> Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Ty  
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 295

Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile  
 1 5 10 15

&lt;210&gt; 296

&lt;211&gt; 259

&lt;212&gt; DNA

&lt;213&gt; Conus rattus

&lt;400&gt; 296

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttgt gtttccgctt 60

actgctcttc cgatggatgg tcatcaacct gcagaccgac ttgttagagcg tatacaggac 120

aacatttcat ctgagcagca tcccttcttt gaaaagagaa gaggctgttg cgcacctccg 180

agaaaatgca aagaccgagc ctgcaaacct gcacgttgct gcggcccagg ataacgtgtt 240

gatgaccaac tttctcgag 259

&lt;210&gt; 297

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus rattus

&lt;400&gt; 297

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Val Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu  
 20 25 30

Val Glu Arg Ile Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe  
 35 40 45

Glu Lys Arg Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg  
 50 55 60

Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly  
 65 70 75

&lt;210&gt; 298

<211> 23  
 <212> PRT  
 <213> Conus rattus

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 298  
 Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys  
 1 5 10 15

Xaa Ala Arg Cys Cys Gly Xaa  
 20

<210> 299  
 <211> 262  
 <212> DNA  
 <213> Conus stercusmuscarum

<400> 299  
 ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt 60  
 attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120  
 gacatttcat ctgagaagca tcccttgttt gataagagac aacggtgttg caatggcgg 180  
 aggggatgct ccagcagatg gtgcagagat cactcacgtt gttgcggctg acgataaacgt 240  
 gttgatgacc aactttctcg ag 262

<210> 300  
 <211> 76  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 300  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Ile Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Lys His Pro Leu Phe  
 35 40 45

Asp Lys Arg Gln Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg  
 50 55 60

Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg  
 65 70 75

<210> 301  
 <211> 22  
 <212> PRT  
 <213> Conus stercusmuscarum

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Trp or  
 bromo-Trp

<400> 301  
 Xaa Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Xaa Cys Arg  
 1 5 10 15

Asp His Ser Arg Cys Cys  
 20

<210> 302  
 <211> 241  
 <212> DNA  
 <213> Conus ebraceus

<400> 302  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60  
 actgctcttc cactggatga aggtcaacct gcagacctac ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttgtttgat cctgtcaaac ggtgttgcga gcagccatgc 180  
 tacatggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga 240  
 g 241

<210> 303  
 <211> 67  
 <212> PRT  
 <213> Conus ebraceus

<400> 303  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Gly Gln Pro Ala Asp Leu Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro  
 50 55 60

Cys Cys Phe  
 65

<210> 304  
 <211> 15  
 <212> PRT  
 <213> Conus ebraceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 304  
 Cys Cys Xaa Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
 1 5 10 15

<210> 305  
 <211> 241  
 <212> DNA  
 <213> Conus ebraceus

<400> 305  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gttccctt 60  
 actgctcttc cactggatga agatcaaccc gcagacccatc ctgcagagcg tatgcaggac 120  
 attgcaactg aacagcatcc cttgttgat cctgtcaaac ggtgctgcgc gcagccatgc 180  
 tacatggat gcatcccttg ttgcttctaa taataacgtg ttgatgacca actttctcga 240  
 g 241

<210> 306  
 <211> 67  
 <212> PRT  
 <213> Conus ebraceus

<400> 306  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Leu Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro  
 50 55 60

Cys Cys Phe  
 65

<210> 307  
 <211> 15  
 <212> PRT  
 <213> Conus ebraceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1  
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty  
 r

<400> 307  
 Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe  
 1 5 10 15

<210> 308  
 <211> 238  
 <212> DNA  
 <213> Conus flavidus

<400> 308  
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gttccctt 60  
 actgctgttc cggtggatgg agatcaaccc gcagaccaggc ctgcagagcg tatgcagaac 120  
 gagcagcatc cttgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata 180  
 tgccggcatgg ctaggtgttg ctcgtcatga taacgtgttg atgaccaact ttctcgag 238

<210> 309  
 <211> 67

&lt;212&gt; PRT

&lt;213&gt; Conus flavidus

&lt;400&gt; 309

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro  
20 25 30Ala Glu Arg Met Gln Asn Glu Gln His 'Pro Leu Phe Asp Gln Lys Arg  
35 40 45Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
50 55 60

Cys Ser Ser

65

&lt;210&gt; 310

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus flavidus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(19)

<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or  
bromo-Trp

&lt;400&gt; 310

Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Ser Ser

&lt;210&gt; 311

&lt;211&gt; 245

&lt;212&gt; DNA

&lt;213&gt; Conus miliaris ,

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(245)

&lt;223&gt; n may be any nucleotide

&lt;400&gt; 311

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60

actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcga ttggccatgc 180

agcgcaggat gctacccttg ttgcttccct taataacgtg ttgatgacca actnangnaa 240

aaaaa 245

&lt;210&gt; 312

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Conus miliaris

&lt;400&gt; 312

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe

1	5	10	15
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Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp  
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro  
 50 55 60

Cys Cys Phe Pro  
 65

<210> 313  
<211> 16  
<212> PRT  
<213> Conus miliaris

<220>  
<221> PEPTIDE  
<222> (1)..(16)  
<223> Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 313  
Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa  
 1 5 10 15

<210> 314  
<211> 230  
<212> DNA  
<213> Conus miliaris

<220>  
<221> misc\_feature  
<222> (1)..(230)  
<223> n may be any nucleotide

<400> 314  
ggatccatga tgtctaaact gggagtggtg ccattcgtct ttctggctct gtttcccctg 60  
gcaacactcc aactggatgc agatcaacct gcagaccgac ctgcgcgtaa aaagggcatt 120  
gcaactaaac ggcattccctt gtctgatcct gtcagagggt gttgccctcc aatgtgcaca 180  
ccatgcttcc cttgctgttt tcgttaataa cgtgttgatg natgtgnan 230

<210> 315  
<211> 66  
<212> PRT  
<213> Conus miliaris

<400> 315  
Met Met Ser Lys Leu Gly Val Val Pro Phe Val Phe Leu Val Leu Phe  
 1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Arg Lys Lys Gly Ile Ala Thr Lys Arg His Pro Leu Ser Asp Pro  
 35 40 45

Val Arg Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys  
 50 55 60

Phe Arg  
 65

<210> 316  
 <211> 16  
 <212> PRT  
 <213> Conus miliaris

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4, 9 and 12 is Pro or Hyp; Xaa at residue 5 is Tyr  
 , 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho  
 -Tyr

<400> 316  
 Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arg  
 1 5 10 15

<210> 317  
 <211> 295  
 <212> DNA  
 <213> Conus ammiralis

<400> 317  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
 gcttctgttt ccccttactg ctcttcgct ggatggagat caacctgcag accaagctgc 120  
 agagcgtatg caggccgagc agcatccctt gtttgatcag aaaagacggt gttgcaggtt 180  
 tccatgcccc gatacttgca gacatttgta ttgcgggtga tgataacgtg ctgatgaccc 240  
 actttgtcat cacggctacg tcaagtgtct aatgaataag taaaatgatt gcagt 295

<210> 318  
 <211> 65  
 <212> PRT  
 <213> Conus ammiralis

<400> 318  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala  
 20 25 30

Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg  
 35 40 45

Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys  
 50 55 60

Gly  
 65

<210> 319  
 <211> 16  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 6 and 8 is Pro or Hyp

<400> 319  
 Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys  
 1 5 10 15

<210> 320  
 <211> 267  
 <212> DNA  
 <213> Conus ammiralis

<400> 320  
 caagagggat cgatagcagt tcatgatgtt taaaactggga gtcttgctga ccatctgtct 60  
 acttctgttt tcccttaatg ctgttccgct ggatggagat caacctgcag accaacctgc 120  
 agagcgtctg ctggacgaca tttcatctga aaataatccc ttttatgatc ccgccaaacg 180  
 gtgttgcatg acttgcttcg gttgcacacc ttgttgtgga tgaccagcct catcaagtgt 240  
 ctaacgaata agtaaaaacga ttgcagt 267

<210> 321  
 <211> 66  
 <212> PRT  
 <213> Conus ammiralis

<400> 321  
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Asn Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Leu Asp Asp Ile Ser Ser Glu Asn Asn Pro Phe Tyr  
 35 40 45

Asp Pro Ala Lys Arg Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys  
 50 55 60

Cys Gly  
 65

<210> 322  
 <211> 12  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 10 is Pro or Hyp

<400> 322  
 Cys Cys Met Thr Cys Phe Gly Cys Thr Xaa Cys Cys  
 1 5 10

<210> 323  
 <211> 294  
 <212> DNA  
 <213> Conus ammiralis

<400> 323  
 caagaaggat cgatagcagt tcatgatgtc taaactggga gccttggta ccatctgtct 60  
 acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120  
 agagcgtctg caggaccgccc ttccaaactga aaatcatccc ttatatgatc ccgtcaaacc 180  
 gtgttgcgat gattcggaat gcgactattc ttgttggcct tgctgtattt tttcataacc 240  
 tttgttatcg cggcctcatc ctatgtcaa atgaataagt aaaacgattt cagt 294

<210> 324  
 <211> 71  
 <212> PRT  
 <213> Conus ammiralis

<400> 324  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys  
 50 55 60

Trp Pro Cys Cys Ile Phe Ser  
 65 70

<210> 325  
 <211> 18  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 325  
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile  
 1 5 10 15

Phe Ser

<210> 326  
 <211> 284  
 <212> DNA  
 <213> Conus ammiralis

<400> 326  
 caagaggat cgatagcagt tcatgatgtt taaactcgga gtcttgcgtc ccatctgtct 60  
 acttctgttt tccctaattg ctgttccgct ggatggagat caacatgcag accaacctgc 120  
 agagcgtctg caggaccgccc ttccaaactga aaatcatccc ttatatgatc ccgtcaaacc 180

gtgttgcagg ttgttatgcc tcagttcaa cccttgggttggatgaccag ctttggttatc 240  
 acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284  
 <210> 327  
 <211> 67  
 <212> PRT  
 <213> Conus ammiralis

<400> 327  
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro  
 50 55 60

Cys Cys Gly  
 65

<210> 328  
 <211> 13  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 11 is Pro or Hyp

<400> 328  
 Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Xaa Cys Cys  
 1 5 10

<210> 329  
 <211> 289  
 <212> DNA  
 <213> Conus ammiralis

<400> 329  
 caagaaggat cgatacgagt tcatgatgtc taaaactggga gccttggat ccatctgtct 60  
 acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacctgc 120  
 agagcgtctg caggaccgca ttccaaactga agatcatccc ttatggatc ccaacaaacg 180  
 gtgttgcgat gattcggaat gcggctattc atgctggcct tgctgttatg gataagcttt 240  
 gttatcgccg cctcatccag tgtcaacgaa taagtaaaac gattgcagt 289

<210> 330  
 <211> 70  
 <212> PRT  
 <213> Conus ammiralis

<400> 330  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe  
 35 40 45

Asp Pro Asn Lys Arg Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys  
 50 55 60

Trp Pro Cys Cys Tyr Gly  
 65 70

<210> 331

<211> 16

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 and 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 331

Cys Cys Asp Asp Ser Xaa Cys Gly Xaa Ser Cys Xaa Xaa Cys Cys Xaa  
 1 5 10 15

<210> 332

<211> 272

<212> DNA

<213> Conus spurius

<400> 332

caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60

gcttctgttt ccacgtactt ctcttccgct ggatggagat caacctgcag tccgatctgc 120

aaagcgtatg cattcatcta tacagcgtcg tttctttgat cccgtcaaac ggtgttgccc 180

tagatgcagc gagtgcaacc cttgttgtgg atgaccagct ttgtcatcgc ggcctcatta 240

agtgtcta at gaataagtaa aatgattgca gt 272

<210> 333

<211> 63

<212> PRT

<213> Conus spurius

<400> 333

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe  
 1 5 10 15

Pro Arg Thr Ser Leu Pro Leu Asp Gly Asp Gln Pro Ala Val Arg Ser  
 20 25 30

Ala Lys Arg Met His Ser Ser Ile Gln Arg Arg Phe Phe Asp Pro Val  
 35 40 45

Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly  
 50 55 60

<210> 334

<211> 12  
 <212> PRT  
 <213> Conus spurius

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 and 10 is Pro or Hyp

<400> 334  
 Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys  
 1 5 10

<210> 335  
 <211> 293  
 <212> DNA  
 <213> Conus omaria

<400> 335  
 caagaggat cgatacgagt tcatgatgtc taaaactggga gtctcggtga ccatctgtct 60  
 acttcttattt tcccttactg ctgttccgct tgatggagat caacatgcag accaacacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180  
 gtgttgcgat gaggaagaat gcagcagtgc atgctggcct tggtgttggg ggtgatcagc 240  
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaatgattgc agt 293

<210> 336  
 <211> 70  
 <212> PRT  
 <213> Conus omaria

<400> 336  
 Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45

Asn Pro Val Lys Arg Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys  
 50 55 60

Trp Pro Cys Cys Trp Gly  
 65 70

<210> 337  
 <211> 16  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4, 5 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 337

Cys Cys Asp Xaa Xaa Xaa Cys Ser Ser Ala Cys Xaa Xaa Cys Cys Xaa  
 1 5 10 15

<210> 338

<211> 293

<212> DNA

<213> Conus omaria

<400> 338

caagaaggat cgatagcagt tcatgatgtc taaaactggga gtcttggta tcatctgtct 60  
 acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacacctgc 120  
 agagcgtatg caggacgaca tttcaactga gcatcatccc ttttatgatc ccgtcaaacg 180  
 gtgttgcag tacgggtgga catgcttgct aggatgcact ccttgcattt gttgaccagt 240  
 tttgttatcg cggcctcgta aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 339

<211> 70

<212> PRT

<213> Conus omaria

<400> 339

Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys  
 1 5 10 15

Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Thr Glu His His Pro Phe Tyr  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly  
 50 55 60

Cys Thr Pro Cys Asp Cys  
 65 70

<210> 340

<211> 17

<212> PRT

<213> Conus omaria

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 340

Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp  
 1 5 10 15

Cys

<210> 341

<211> 290

<212> DNA

<213> Conus omaria

<400> 341

caagaggat cgatagcagt tcatgatgtc tatactggga gtcttggta tcatctgtct 60  
 acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120  
 agagcgtatg caggacggca tttcatctga acatcatccc tttttggatc ccgtcaaacg 180  
 gtgttgcatt ctattggcat gcccgttgg atgctgcct tggatcgggtt gaccagctt 240  
 gttatcgccc cctcatcaag tgtctaatga ataagtaaaa cgattgcagt 290  
  
 <210> 342  
 <211> 69  
 <212> PRT  
 <213> Conus omaria  
  
 <400> 342  
 Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys  
 1 5 10 15  
  
 Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30  
  
 Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu  
 35 40 45  
  
 Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys  
 50 55 60  
  
 Ser Pro Cys Cys Trp  
 65  
  
 <210> 343  
 <211> 16  
 <212> PRT  
 <213> Conus omaria  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or brom  
 o-Trp  
  
 <400> 343  
 Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa  
 1 5 10 15  
  
 <210> 344  
 <211> 293  
 <212> DNA  
 <213> Conus omaria  
  
 <400> 344  
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggta tcatctgtct 60  
 acttctttgt ccccttactg ctgttccgca ggatggagat caacctgcag accgacctgc 120  
 agagcgtatg cagggcggca tttcatctga acatcatccc tttttggatc ccgtcaaacg 180  
 gtgttgcagg tacgggtgga catgctggct agatgcact ccctgtgggtt gttgaccagc 240  
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293  
  
 <210> 345  
 <211> 70

&lt;212&gt; PRT

&lt;213&gt; Conus omaria

&lt;400&gt; 345

Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys  
1 5 10 15Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe  
35 40 45Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly  
50 55 60Cys Thr Pro Cys Gly Cys  
65 70

&lt;210&gt; 346

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus omaria

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(17)

<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or  
bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 346

Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly  
1 5 10 15

Cys

&lt;210&gt; 347

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Conus episcopatus

&lt;400&gt; 347

caagaaggat cgatagcagt tcatgatgtc taaaactggga gtcttggta ccatctgtct 60

acttctgttt tcccttattt ctgttccgct tggatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatattatgc ctgtcaaacg 180

gtgttgcgtt gaggacgaat gcaacagttc atgctggcct tggatgggg ggtgatcagc 240

tttgcgttatacg cggcctgtatc aagtgtataa tgaataagta aaacgattgc agt 293

&lt;210&gt; 348

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Conus episcopatus

&lt;400&gt; 348

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro

20

25

30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45

Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys  
 50 55 60

Trp Pro Cys Cys Trp Gly  
 65 70

<210> 349  
 <211> 16  
 <212> PRT  
 <213> Conus episcopatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 349  
 Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa  
 1 5 10 15

<210> 350  
 <211> 293  
 <212> DNA  
 <213> Conus episcopatus

<400> 350  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgtct 60  
 acttctgttt tcccttattt ctgttccgct tggatggagat caacatgcag accaacctgc 120  
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatattgc ctgtcaaacg 180  
 gtgttgcgat gaggacgaat gcagcagttc atgctggcct tggatgggg gatgagcagc 240  
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 351  
 <211> 70  
 <212> PRT  
 <213> Conus episcopatus

<400> 351  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Phe  
 1 5 10 15

Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45

Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys  
 50 55 60

Trp Pro Cys Cys Trp Gly  
 65 70

&lt;210&gt; 352

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus episcopatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

&lt;223&gt; Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

&lt;400&gt; 352

Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa  
1 5 10 15

&lt;210&gt; 353

&lt;211&gt; 290

&lt;212&gt; DNA

&lt;213&gt; Conus episcopatus

&lt;400&gt; 353

caagagggat cgatagcagt tcatgatgtc taaaactggga gtcttggta ccatctgtct 60  
acttctgttt tcccttactg ctgttccgct tggatggagat caacatgcag accaacctgc 120  
agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatattaatc ccgtcaaacg 180  
gtgttgcggc gccccatgtgcatggg atgcaaggct tggatggat gagcagctt 240  
gttatcgtgg cctcatcaag tgtctaata 15 290  
ataagtaaaa cgattgcagt

&lt;210&gt; 354

&lt;211&gt; 69

&lt;212&gt; PRT

&lt;213&gt; Conus episcopatus

&lt;400&gt; 354

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
20 25 30Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
35 40 45Asn Pro Val Lys Arg Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys  
50 55 60Lys Pro Cys Cys Gly  
65

&lt;210&gt; 355

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Conus episcopatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(15)

&lt;223&gt; Xaa at residue 3 and 13 is Pro or Hyp

&lt;400&gt; 355

Cys Cys Xaa Ala Ala Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys  
 1 5 10 15

<210> 356

<211> 295

<212> DNA

<213> Conus aulicus

<400> 356

caagagggat cgatagcagt tcatgatgtc taaaactggga gtcttggta ccatctgtct 60  
 gcttctgttt tccgttactg ctcttccgcc ggatggagat caacctgcag accgagctgc 120  
 agagcgtagg caggtcgagc agcatcccggt gtttgatcat gaaagagggt gttgctcgcc 180  
 accatgccac agtatttgcg ctgctttctg ttgcgggtga tgataaacgtg ttgatgaccc 240  
 actttgtcat cacggctgcg tcaagtgtct aatgaataag taaaatgatt gcagt 295

<210> 357

<211> 65

<212> PRT

<213> Conus aulicus

<400> 357

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Val Thr Ala Leu Pro Pro Asp Gly Asp Gln Pro Ala Asp Arg Ala  
 20 25 30

Ala Glu Arg Arg Gln Val Glu Gln His Pro Val Phe Asp His Glu Arg  
 35 40 45

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys  
 50 55 60

Gly

65

<210> 358

<211> 16

<212> PRT

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 5 and 6 is Pro or Hyp

<400> 358

Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys  
 1 5 10 15

<210> 359

<211> 290

<212> DNA

<213> Conus aulicus

<400> 359

caagagggat cgatagcagt tcatgatgtc taaaactggga gtcttggta ccatctgtct 60  
 actttctgttt tccgttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120

agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatthaatc ccgtcaaacg 180  
 gtgttgccga ccgggtggcat gtgccatggg atgcaagcct tgttgtggat gagcagctt 240  
 gttatcgtgg cctcatcaag tgtctaata 180  
  
 <210> 360  
 <211> 69  
 <212> PRT  
 <213> Conus aulicus  
  
 <400> 360  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30  
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe  
 35 40 45  
 Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys  
 50 55 60  
 Lys Pro Cys Cys Gly  
 65  
  
 <210> 361  
 <211> 15  
 <212> PRT  
 <213> Conus aulicus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 4 and 13 is Pro or Hyp  
  
 <400> 361  
 Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys  
 1 5 10 15  
  
 <210> 362  
 <211> 290  
 <212> DNA  
 <213> Conus aulicus  
  
 <400> 362  
 caagagggat cgatagcgt tcatgatgtc taaactggga gtcttggat tcatctgtct 60  
 acttctgtct ccccttactg ctgttccgct ggatggagat caacctgcag accgacctgc 120  
 agagcgtatg caggacgaca tttcatctga acatcaaccc atgttgcgt ccacatcagaca 180  
 gtgttgcccg gcgggtggcat ggcgcatggg atgcgaccc tggtgtggat gaccagctt 240  
 gttatcgcgg cctcatcaag tgtctaata 290  
  
 <210> 363  
 <211> 69  
 <212> PRT  
 <213> Conus aulicus  
  
 <400> 363  
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Ser

1	5	10	15
---	---	----	----

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro  
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His Gln Pro Met Phe  
 35 40 45

Asp Ala Ile Arg Gln Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys  
 50 55 60

Glu Pro Cys Cys Gly  
 65

<210> 364  
<211> 16  
<212> PRT  
<213> Conus aulicus

<220>  
<221> PEPTIDE  
<222> (1)..(16)  
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 13 is Glu or  
 gamma-carboxy Glu; Xaa at residue 4 and 14 is Pro or Hyp

<400> 364  
Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys  
 1 5 10 15

<210> 365  
<211> 293  
<212> DNA  
<213> Conus aureus

<400> 365  
caagaaggat cgatagcagt tcatgatgtc taaaactggga gccttggta ccatctgtct 60  
acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacatgc  
agagcgtctg catgaccgccc ttccaactga aaatcatccc ttatatgatc coggtaaacc 120  
gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtatcc ttggataacc  
tttggatcg cggcctcatc aagtgtcaaa tgaataagta aaacgattgc agt 180  
240  
293

<210> 366  
<211> 71  
<212> PRT  
<213> Conus aureus

<400> 366  
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln His  
 20 25 30

Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr  
 35 40 45

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys  
 50 55 60

Trp Pro Cys Cys Ile Phe Gly

65 70

<210> 367  
 <211> 17  
 <212> PRT  
 <213> Conus aureus

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 367  
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile  
 1 5 10 15

Phe

<210> 368  
 <211> 290  
 <212> DNA  
 <213> Conus aureus

<400> 368  
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggta ccatctgtct 60  
 acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc  
 agagcgtctg caggaccgca ttccaaactga aaatcatccc ttatttgcata cgaacaaacg 120  
 gtgttgcaat gattggaaat ggcacgattc atgctggcct tgctgttatg gataaccttt 180  
 gttatcgcgg cctccatcaag tgtcaaatga ataagtaaaa cgattgcagt 240  
 290

<210> 369  
 <211> 70  
 <212> PRT  
 <213> Conus aureus

<400> 369  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro  
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe  
 35 40 45

Asp Pro Asn Lys Arg Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys  
 50 55 60

Trp Pro Cys Cys Tyr Gly  
 65 70

<210> 370  
 <211> 16  
 <212> PRT  
 <213> Conus aureus

<220>

<221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 5 and 12 is Trp or bromo-Trp; Xaa at residue 16 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 370  
 Cys Cys Asn Asp Xaa Xaa Cys Asp Asp Ser Cys Xaa Xaa Cys Cys Xaa  
 1 5 10 15

<210> 371  
 <211> 310  
 <212> DNA  
 <213> Conus consors

<400> 371  
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggta ccatctgttt 60  
 gcttcgttt ccccttactg ctcttccaaat ggatggagat caatctgttag accgacactgc 120  
 agagcgtatg caggacgaca tttcatctga gctgcattccc ttgttcaatc agaaaagaat 180  
 gtgttgcggc gaagggtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg 240  
 ttgttaaatg acaacgtgtc gatgaccaac ttctgttatca cgactaatga ataagtaaaa 300  
 tgattgcagt 310

<210> 372  
 <211> 74  
 <212> PRT  
 <213> Conus consors

<400> 372  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro  
 20 25 30  
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Phe  
 35 40 45  
 Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr  
 50 55 60

Phe Arg Asn Ser Gln Ile Cys His Cys Cys  
 65 70

<210> 373  
 <211> 22  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 373  
 Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser

1

5

10

15

Gln Ile Cys His Cys Cys  
20

&lt;210&gt; 374

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Conus consors

&lt;400&gt; 374

taagagggat cgatagcagt tcatgatgtc taaaactggga gtcttggta ccatctgtct 60  
gcttctgttt ccccttattt ctcttccaat ggatggagat caacctgcag accgacacctgc  
agagcgtatg caggacgaca tttcatctca gcagcatccc ttgtttgata agagaggccg 120  
ctgttgcgtatg gtgccgaacg catgctccgg cagatggtgc agagatcacg cacaatgttg  
cggatgacga taacgtgttg atgaccaact ttgtgatcac ggctacatca agtgaataag 180  
taaaacgatt gcagt 240  
300  
315

&lt;210&gt; 375

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;400&gt; 375

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
1 5 10 15

Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe  
35 40 45

Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg  
50 55 60

Trp Cys Arg Asp His Ala Gln Cys Cys Gly  
65 70

&lt;210&gt; 376

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(22)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo  
-Trp

&lt;400&gt; 376

Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg  
1 5 10 15

Asp His Ala Gln Cys Cys  
20

&lt;210&gt; 377

&lt;211&gt; 322

&lt;212&gt; DNA

&lt;213&gt; Conus consors

&lt;400&gt; 377

caagagggat cgatacgagt tcatacgatgtc taaaactggga gtcttggttga ctgtctgttt 60  
 gcttcgttt ccccttactg ctcttccgat ggatggagat caacctgcag accaacctgc 120  
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttgata agagacaaag 180  
 gtgttgcact gggaaagaagg ggtcatgctc cggttaaagca tgcaaaagtc tcaaatgtt 240  
 ctctggacga taacgtgtt atgaccaact ttgttatacac ggctacgtca agtgtctagt 300  
 gaataagtaa aacgattgca gt 322

&lt;210&gt; 378

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;400&gt; 378

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Val	Cys	Leu	Leu	Phe
1				5				10					15	

Pro	Leu	Thr	Ala	Leu	Pro	Met	Asp	Gly	Asp	Gln	Pro	Ala	Asp	Gln	Pro
20					25						30				

Ala	Glu	Arg	Met	Gln	Asp	Asp	Ile	Ser	Ser	Glu	Gln	His	Pro	Leu	Phe
35					40					45					

Asp	Lys	Arg	Gln	Arg	Cys	Cys	Thr	Gly	Lys	Lys	Gly	Ser	Cys	Ser	Gly
50					55				60						

Lys	Ala	Cys	Lys	Ser	Leu	Lys	Cys	Cys	Ser	Gly	Arg
65				70					75		

&lt;210&gt; 379

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(23)

&lt;223&gt; Xaa at residue 1 is Gln or pyro-Glu

&lt;400&gt; 379

Xaa	Arg	Cys	Cys	Thr	Gly	Lys	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5			10			15					

Lys	Ser	Leu	Lys	Cys	Cys	Ser
		20				

&lt;210&gt; 380

&lt;211&gt; 284

&lt;212&gt; DNA

&lt;213&gt; Conus emaciatus

&lt;400&gt; 380

caagagggat	cgatacgagt	tcatacgatgtc	taaaactggga	gtcttggttga	ccatctgtct	60
------------	------------	--------------	-------------	-------------	------------	----

gcttcgttt	cccttactg	ttcttccgat	ggatggagat	caacctgcag	acctacactgc	120
-----------	-----------	------------	------------	------------	-------------	-----

attgcgtgcg cagttcttg cacctgaaca tagtccccgg tttgaccccg tcaaacggtg 180  
 ctgctcgccg gattgcagtg tttgcatccc ttgttgcccg tatggatcac ctgattatt 240  
 gcggccacgt caagtgtcta atgaataagt aaaatgattg cagt 284  
  
 <210> 381  
 <211> 70  
 <212> PRT  
 <213> Conus emaciatus  
  
 <400> 381  
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1 5 10 15  
  
 Pro Leu Thr Val Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Leu Pro  
 20 25 30  
  
 Ala Leu Arg Ala Gln Phe Phe Ala Pro Glu His Ser Pro Arg Phe Asp  
 35 40 45  
  
 Pro Val Lys Arg Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys  
 50 55 60  
  
 Cys Pro Tyr Gly Ser Pro  
 65 70  
  
 <210> 382  
 <211> 18  
 <212> PRT  
 <213> Conus emaciatus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(18)  
 <223> Xaa at residue 11, 14 and 18 is Pro or Hyp; Xaa at residue 15 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos  
 pho-Tyr  
  
 <400> 382  
 Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Xaa Cys Cys Xaa Xaa Gly  
 1 5 10 15  
  
 Ser Xaa  
  
 <210> 383  
 <211> 13  
 <212> PRT  
 <213> Conus aurisiacus  
  
 <400> 383  
 Cys Cys Lys Val Gln Cys Glu Ser Cys Thr Pro Cys Cys  
 1 5 10  
  
 <210> 384  
 <211> 15  
 <212> PRT  
 <213> Conus atlanticus  
  
 <400> 384  
 Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys  
 1 5 10 15

<210> 385  
 <211> 14  
 <212> PRT  
 <213> Conus arentus

<400> 385  
 Cys Cys Glu Arg Pro Cys Asn Ile Gly Cys Val Pro Cys Cys  
 1 5 10

<210> 386  
 <211> 16  
 <212> PRT  
 <213> Conus bandus

<400> 386  
 Cys Cys Asn Trp Pro Cys Ser Met Gly Cys Ile Pro Cys Cys Tyr Tyr  
 1 5 10 15

<210> 387  
 <211> 15  
 <212> PRT  
 <213> Conus betulinus

<400> 387  
 Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys Cys Trp Pro  
 1 5 10 15

<210> 388  
 <211> 16  
 <212> PRT  
 <213> Conus betulinus

<400> 388  
 Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys Cys Trp Pro Ser  
 1 5 10 15

<210> 389  
 <211> 18  
 <212> PRT  
 <213> Conus betulinus

<400> 389  
 Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro Cys Cys Pro Asn Trp  
 1 5 10 15

Pro Ala

<210> 390  
 <211> 14  
 <212> PRT  
 <213> Conus betulinus

<400> 390  
 Cys Cys Lys Gln Ser Cys Thr Thr Cys Met Pro Cys Cys Trp  
 1 5 10

<210> 391  
 <211> 14  
 <212> PRT  
 <213> Conus betulinus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa is Glu or gamma-carboxy Glu

&lt;400&gt; 391

Ala	Cys	Cys	Xaa	Gln	Ser	Cys	Thr	Thr	Cys	Met	Pro	Cys	Cys
1				5									

&lt;210&gt; 392

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus betulinus

&lt;400&gt; 392

Cys	Cys	Glu	Gln	Ser	Cys	Thr	Thr	Cys	Met	Pro	Cys	Cys	Trp
1				5									

&lt;210&gt; 393

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;400&gt; 393

Arg	Cys	Cys	Arg	Tyr	Pro	Cys	Pro	Asp	Ser	Cys	His	Gly	Ser	Cys	Cys
1				5					10						15

Tyr Lys

&lt;210&gt; 394

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;400&gt; 394

Cys	Cys	Pro	Pro	Val	Ala	Cys	Asn	Met	Gly	Cys	Lys	Pro	Cys	Cys
1				5					10					15

&lt;210&gt; 395

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;400&gt; 395

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Met
1				5					10						15

Phe

&lt;210&gt; 396

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;400&gt; 396

Cys	Cys	Arg	Arg	Cys	Tyr	Met	Gly	Cys	Ile	Pro	Cys	Cys	Phe
1				5					10				

&lt;210&gt; 397

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 397

Cys	Cys	Pro	Pro	Val	Ala	Cys	Asn	Met	Gly	Cys	Lys	Pro	Cys	Cys	Gly
1				5					10						15

<210> 398  
 <211> 19  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Xaa is Hyp

<400> 398  
 Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa  
 1 5 10 15

Cys Cys Asn

<210> 399  
 <211> 15  
 <212> PRT  
 <213> Conus capitaneus

<400> 399  
 Ser Cys Cys Arg Asp Cys Gly Glu Asp Cys Val Gly Cys Cys Arg  
 1 5 10 15

<210> 400  
 <211> 16  
 <212> PRT  
 <213> Conus coronatus

<400> 400  
 Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro Cys Cys Leu Pro  
 1 5 10 15

<210> 401  
 <211> 18  
 <212> PRT  
 <213> Conus dalli

<400> 401  
 Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile  
 1 5 10 15

Leu Ser

<210> 402  
 <211> 17  
 <212> PRT  
 <213> Conus dalli

<400> 402  
 Glx Gln Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Glu Pro Cys  
 1 5 10 15

Cys

<210> 403  
 <211> 16  
 <212> PRT  
 <213> Conus dalli

<400> 403  
 Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Pro Cys Cys Trp  
 1 5 10 15

<210> 404

<211> 14

<212> PRT

<213> Conus distans

<400> 404

Glx Cys Cys Val His Pro Cys Pro Cys Thr Pro Cys Cys Arg  
1 5 10

<210> 405

<211> 14

<212> PRT

<213> Conus figulinus

<400> 405

Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val Pro Cys Cys  
1 5 10

<210> 406

<211> 14

<212> PRT

<213> Conus figulinus

<400> 406

Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro Cys Cys Pro  
1 5 10

<210> 407

<211> 15

<212> PRT

<213> Conus figulinus

<400> 407

Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu  
1 5 10 15

<210> 408

<211> 16

<212> PRT

<213> Conus figulinus

<400> 408

Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro Cys Cys Thr Ser  
1 5 10 15

<210> 409

<211> 16

<212> PRT

<213> Conus figulinus

<400> 409

Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro Cys Cys Ile Pro  
1 5 10 15

<210> 410

<211> 16

<212> PRT

<213> Conus generalis

<400> 410

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro  
1 5 10 15

<210> 411

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus generalis

&lt;400&gt; 411

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Leu Thr  
1 5 10 15

&lt;210&gt; 412

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus generalis

&lt;400&gt; 412

Glx Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro  
1 5 10 15

&lt;210&gt; 413

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus gloriamaris

&lt;400&gt; 413

Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Met  
1 5 10 15

Phe

&lt;210&gt; 414

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus gloriamaris

&lt;400&gt; 414

Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys  
1 5 10 15

Trp

&lt;210&gt; 415

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus gloriamaris

&lt;400&gt; 415

Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys Gly  
1 5 10 15

&lt;210&gt; 416

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Conus laterculatus

&lt;400&gt; 416

Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys Cys  
1 5 10

&lt;210&gt; 417

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus leopardus

&lt;400&gt; 417

Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr Cys Arg His Gln

1

5

10

15

Cys Cys His

&lt;210&gt; 418

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus lividus

&lt;400&gt; 418

Glx Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser Cys His Tyr Gln  
1 5 10 15

Cys Cys His

&lt;210&gt; 419

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 419

Cys Cys Arg Leu Ser Cys Gly Leu Gly Cys His Pro Cys Cys  
1 5 10

&lt;210&gt; 420

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 420

Glu Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Pro Cys Cys  
1 5 10 15

Val

&lt;210&gt; 421

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 421

Ser Lys Gln Cys Cys His Leu Pro Ala Cys Arg Phe Gly Cys Thr Pro  
1 5 10 15

Cys Cys Trp

&lt;210&gt; 422

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 422

Met Gly Cys Cys Pro Phe Pro Cys Lys Thr Ser Cys Thr Thr Leu Cys  
1 5 10 15

Cys

&lt;210&gt; 423

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus musicus

&lt;400&gt; 423

Ala Cys Cys Glu Gln Ser Cys Thr Thr Cys Phe Pro Cys Cys

1	5	10
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<210> 424  
 <211> 15  
 <212> PRT  
 <213> Conus nobilis

<400> 424  
 Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe Cys Val Pro Cys Cys  
 1 5 10 15

<210> 425  
 <211> 14  
 <212> PRT  
 <213> Conus pulicarius

<400> 425  
 Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
 1 5 10

<210> 426  
 <211> 17  
 <212> PRT  
 <213> Conus quercinus

<400> 426  
 Glx Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg  
 1 5 10 15

Thr

<210> 427  
 <211> 18  
 <212> PRT  
 <213> Conus quercinus

<400> 427  
 Glx Arg Cys Cys Arg Trp Pro Cys Pro Gly Ser Cys Arg Cys Cys Arg  
 1 5 10 15

Tyr Arg

<210> 428  
 <211> 18  
 <212> PRT  
 <213> Conus quercinus

<400> 428  
 Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser Cys His Gly Ser Cys Cys  
 1 5 10 15

Tyr Lys

<210> 429  
 <211> 15  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa is Hyp

<400> 429

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn  
 1 5 10 15

<210> 430  
 <211> 15  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa is Hyp

<400> 430  
 Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn  
 1 5 10 15

<210> 431  
 <211> 16  
 <212> PRT  
 <213> Conus rattus

<400> 431  
 Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln  
 1 5 10 15

<210> 432  
 <211> 20  
 <212> PRT  
 <213> Conus striatus

<400> 432  
 Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His  
 1 5 10 15

Ala Arg Cys Cys  
 20

<210> 433  
 <211> 12  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa is Hyp

<400> 433  
 Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys  
 1 5 10

<210> 434  
 <211> 14  
 <212> PRT  
 <213> Conus tessulatus

<400> 434  
 Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile  
 1 5 10

<210> 435  
 <211> 18  
 <212> PRT

<213> Conus tessulatus

<400> 435

Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Tyr

<210> 436

<211> 23

<212> PRT

<213> Conus betulinus

<400> 436

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Phe Val Met Ile Thr Cys  
20

<210> 437

<211> 23

<212> PRT

<213> Conus betulinus

<400> 437

Arg Cys Cys Arg Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Phe Val Met Ile Thr Cys  
20

<210> 438

<211> 15

<212> PRT

<213> Conus textile

<400> 438

Phe Cys Cys Asp Ser Asn Trp Cys His Asp Cys Glu Cys Cys Tyr  
1 5 10 15

<210> 439

<211> 16

<212> PRT

<213> Conus marmoreus

<400> 439

Cys Cys His Trp Asn Trp Cys Asp His Leu Cys Ser Cys Cys Gly Ser  
1 5 10 15

<210> 440

<211> 16

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa is Hyp

<400> 440

Asp Cys Cys Xaa Leu Pro Ala Cys Pro Phe Gly Cys Asn Xaa Cys Cys  
1 5 10 15

&lt;210&gt; 441

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 441

Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Cys Arg  
1 5 10 15

&lt;210&gt; 442

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(16)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 442

Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Cys Arg  
1 5 10 15

&lt;210&gt; 443

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;400&gt; 443

Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Cys Arg  
1 5 10 15

&lt;210&gt; 444

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus marmoreus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(17)

&lt;223&gt; Xaa is Hyp

&lt;400&gt; 444

Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys  
1 5 10 15

Val

&lt;210&gt; 445

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 445

Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys  
1 5 10 15

&lt;210&gt; 446

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 446

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu Cys Cys  
1 5 10 15

&lt;210&gt; 447

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus aureus

&lt;400&gt; 447

Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile  
1 5 10 15

Phe

&lt;210&gt; 448

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus aureus

&lt;400&gt; 448

Cys Cys Asn Asp Trp Glu Cys Asp Asp Ser Cys Trp Pro Cys Cys Tyr  
1 5 10 15

&lt;210&gt; 449

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 449

Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys  
1 5 10 15

&lt;210&gt; 450

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 450

Cys Cys Met Thr Cys Phe Gly Cys Thr Pro Cys Cys  
1 5 10

&lt;210&gt; 451

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 451

Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile  
1 5 10 15

Phe Ser

&lt;210&gt; 452

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 452

Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro Cys Cys  
1 5 10

<210> 453

<211> 16

<212> PRT

<213> Conus ammiralis

<400> 453

Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys Trp Pro Cys Cys Tyr  
1 5 10 15

<210> 454

<211> 16

<212> PRT

<213> Conus aulicus

<400> 454

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys  
1 5 10 15

<210> 455

<211> 15

<212> PRT

<213> Conus aulicus

<400> 455

Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys Lys Pro Cys Cys  
1 5 10 15

<210> 456

<211> 16

<212> PRT

<213> Conus aulicus

<400> 456

Glx Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys Glu Pro Cys Cys  
1 5 10 15

<210> 457

<211> 18

<212> PRT

<213> Conus emaciatus

<400> 457

Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys Cys Pro Tyr Gly  
1 5 10 15

Ser Pro

<210> 458

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 458

Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp  
1 5 10 15

<210> 459

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 459

Cys Cys Asp Glu Asp Glu Cys Ser Ser Cys Trp Pro Cys Cys Trp  
1 5 10 15

<210> 460  
<211> 15  
<212> PRT  
<213> *Conus episcopatus*

<400> 460  
Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys Lys Pro Cys Cys  
1 5 10 15

<210> 461  
<211> 16  
<212> PRT  
<213> *Conus omaria*

<400> 461  
Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp  
1 5 10 15

<210> 462  
<211> 16  
<212> PRT  
<213> *Conus omaria*

<400> 462  
Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys Trp  
1 5 10 15

<210> 463  
<211> 12  
<212> PRT  
<213> *Conus spurius*

<400> 463  
Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys  
1 5 10

<210> 464  
<211> 16  
<212> PRT  
<213> *Conus pennaceus*

<400> 464  
Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys  
1 5 10 15

<210> 465  
<211> 19  
<212> PRT  
<213> *Conus flavidus*

<400> 465  
Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys  
1 5 10 15

Cys Ser Ser

<210> 466  
<211> 14  
<212> PRT  
<213> *Conus pulicarius*

<400> 466  
Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys Cys His Ile  
1 5 10

<210> 467  
 <211> 15  
 <212> PRT  
 <213> Conus ebraceus

<400> 467  
 Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
 1 5 10 15

<210> 468  
 <211> 15  
 <212> PRT  
 <213> Conus ebraceus

<400> 468  
 Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
 1 5 10 15

<210> 469  
 <211> 14  
 <212> PRT  
 <213> Conus pulicarius

<400> 469  
 Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe  
 1 5 10

<210> 470  
 <211> 16  
 <212> PRT  
 <213> Conus miliaris

<400> 470  
 Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro Cys Cys Phe Pro  
 1 5 10 15

<210> 471  
 <211> 16  
 <212> PRT  
 <213> Conus miliaris

<400> 471  
 Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys Phe Arg  
 1 5 10 15

<210> 472  
 <211> 23  
 <212> PRT  
 <213> Conus rattus

<400> 472  
 Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys  
 1 5 10 15

Pro Ala Arg Cys Cys Gly Pro  
 20

<210> 473  
 <211> 22  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 473  
 Glx Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Trp Cys Arg

1

5

10

15

Asp His Ser Arg Cys Cys  
20

&lt;210&gt; 474

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;400&gt; 474

Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg  
1 5 10 15

Asp His Ala Gln Cys Cys  
20

&lt;210&gt; 475

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus consors

&lt;400&gt; 475

Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
1 5 10 15

Lys Ser Leu Lys Cys Cys Ser  
20

&lt;210&gt; 476

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 476

Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser  
1 5 10 15

Gln Ile Cys His Cys Cys  
20

&lt;210&gt; 477

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Conus aurisiacus

&lt;400&gt; 477

Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly  
1 5 10 15

Cys Cys Leu

&lt;210&gt; 478

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus bullatus

&lt;400&gt; 478

Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser  
1 5 10 15

Gln Ile Cys Ala Cys Cys  
20

<210> 479  
 <211> 21  
 <212> PRT  
 <213> *Conus characteristicus*

<400> 479  
 Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe  
 1 5 10 15

Ile Cys Gly Cys Cys  
 20

<210> 480  
 <211> 23  
 <212> PRT  
 <213> *Conus circumcisus*

<400> 480  
 Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr Phe Lys Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 481  
 <211> 20  
 <212> PRT  
 <213> *Conus ermineus*

<400> 481  
 Cys Cys Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys  
 1 5 10 15

Phe Cys Cys Leu  
 20

<210> 482  
 <211> 21  
 <212> PRT  
 <213> *Conus magus*

<400> 482  
 Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp Asn Phe  
 1 5 10 15

Ile Cys Gly Cys Cys  
 20

<210> 483  
 <211> 22  
 <212> PRT  
 <213> *Conus magus*

<400> 483  
 Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser  
 1 5 10 15

Gln Ile Cys His Cys Cys  
 20

<210> 484  
 <211> 22  
 <212> PRT  
 <213> *Conus magus*

<400> 484  
 Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Thr Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys  
 20

<210> 485  
 <211> 23  
 <212> PRT  
 <213> Conus magus

<400> 485  
 Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 486  
 <211> 23  
 <212> PRT  
 <213> Conus striatus

<400> 486  
 Glx Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe Lys Asn  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 487  
 <211> 22  
 <212> PRT  
 <213> Conus magus

<400> 487  
 Glx Lys Cys Cys Ser Gly Gly Ser Cys Pro Leu Tyr Phe Arg Asp Arg  
 1 5 10 15

Leu Ile Cys Pro Cys Cys  
 20

<210> 488  
 <211> 23  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 488  
 Glx Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe Lys Asp  
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys  
 20

<210> 489  
 <211> 22  
 <212> PRT  
 <213> Conus consors

<400> 489  
 Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser  
 1 5 10 15

Gln Ile Cys His Cys Cys  
20

<210> 490  
<211> 23  
<212> PRT  
<213> Conus aurisiacus

<400> 490  
Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
20

<210> 491  
<211> 23  
<212> PRT  
<213> Conus aurisiacus

<400> 491  
Glx Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys  
1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
20

<210> 492  
<211> 23  
<212> PRT  
<213> Conus bullatus

<400> 492  
Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly Arg Trp Cys  
1 5 10 15

Arg Asp His Ser Arg Cys Cys  
20

<210> 493  
<211> 23  
<212> PRT  
<213> Conus bullatus

<400> 493  
Val Gly Asp Arg Cys Cys Lys Gly Lys Arg Gly Cys Gly Arg Trp Cys  
1 5 10 15

Arg Asp His Ser Arg Cys Cys  
20

<210> 494  
<211> 24  
<212> PRT  
<213> Conus bullatus

<400> 494  
Val Gly Glu Arg Cys Cys Lys Asn Gly Lys Arg Gly Cys Gly Arg Trp  
1 5 10 15

Cys Arg Asp His Ser Arg Cys Cys  
20

<210> 495

<211> 26  
 <212> PRT  
 <213> Conus bullatus

<400> 495  
 Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser  
 1 5 10 15  
 Arg Trp Cys Arg Asp His Ser Arg Cys Cys  
 20 25

<210> 496  
 <211> 25  
 <212> PRT  
 <213> Conus bullatus

<400> 496  
 Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp Arg  
 1 5 10 15  
 Trp Cys Glu Lys Asn Ser Arg Cys Cys  
 20 25

<210> 497  
 <211> 22  
 <212> PRT  
 <213> Conus characteristicus

<400> 497  
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys  
 1 5 10 15  
 Pro Gln Arg Cys Cys Ala  
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<210> 498  
 <211> 23  
 <212> PRT  
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<400> 498  
 Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp Arg Ala Cys  
 1 5 10 15  
 Lys Pro Gln Arg Cys Cys Gly  
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<210> 499  
 <211> 22  
 <212> PRT  
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<400> 499  
 Glx Arg Leu Cys Cys Gly Phe Pro Lys Ser Cys Arg Ser Arg Gln Cys  
 1 5 10 15  
 Lys Pro His Arg Cys Cys  
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<210> 500  
 <211> 22  
 <212> PRT  
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<400> 500  
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys  
 1 5 10 15

Pro Ala Arg Cys Cys Gly  
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<210> 501  
 <211> 22  
 <212> PRT  
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<400> 501  
 Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys  
 1 5 10 15

Met Arg Lys Ala Cys Cys  
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<210> 502  
 <211> 22  
 <212> PRT  
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<400> 502  
 Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys Glu Ser Cys  
 1 5 10 15

Lys Arg Lys Ala Cys Cys  
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<210> 503  
 <211> 22  
 <212> PRT  
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<220>  
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 <222> (1)..(22)  
 <223> Xaa is Hyp

<400> 503  
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Xaa Gln Arg Cys Cys Ala  
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<210> 504  
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<220>  
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<400> 504  
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Xaa Met Lys Cys Cys Ala  
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<210> 505  
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 <212> PRT  
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<220>  
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 <222> (1)..(22)  
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<400> 505  
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 1 5 10 15

Xaa Leu Lys Cys Cys Ala  
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<210> 506  
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 <212> PRT  
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<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
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<400> 506  
 Glx Arg Leu Cys Cys Gly Phe Xaa Lys Ser Cys Arg Ser Arg Gln Cys  
 1 5 10 15

Lys Xaa His Arg Cys Cys  
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<210> 507  
 <211> 22  
 <212> PRT  
 <213> Conus magus

<400> 507  
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys  
 1 5 10 15

Pro Gln Arg Cys Cys Ala  
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<210> 508  
 <211> 24  
 <212> PRT  
 <213> Conus marmoreus

<400> 508  
 Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys  
 1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro  
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<210> 509  
 <211> 23  
 <212> PRT  
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<400> 509

Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys  
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
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<210> 510  
 <211> 24  
 <212> PRT  
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<400> 510  
 Arg Gly Gly Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Ala Cys  
 1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro  
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<210> 511  
 <211> 23  
 <212> PRT  
 <213> Conus parius

<400> 511  
 Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys  
 1 5 10 15

Pro Ala Arg Cys Cys Gly Pro  
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<210> 512  
 <211> 24  
 <212> PRT  
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<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa is Hyp

<400> 512  
 Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala  
 1 5 10 15

Cys Lys Arg Asn Xaa Cys Cys Thr  
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<210> 513  
 <211> 24  
 <212> PRT  
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<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa is Hyp

<400> 513  
 Glx Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys  
 1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser  
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<210> 514  
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 <212> PRT  
 <213> Conus radiatus

<400> 514  
 Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys  
 1 5 10 15

Lys Pro Ala Arg Cys Cys Gly Pro  
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<210> 515  
 <211> 23  
 <212> PRT  
 <213> Conus stercusmuscarum

<400> 515  
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 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser  
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<210> 516  
 <211> 21  
 <212> PRT  
 <213> Conus tulipa

<220>  
 <221> PEPTIDE  
 <222> (1)..(21)  
 <223> Xaa is Hyp

<400> 516

His Gly Cys Cys Lys Gly Xaa Glu Gly Cys Ser Ser Arg Glu Cys Arg  
 1 5 10 15

Xaa Gln His Cys Cys  
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<210> 517  
 <211> 21  
 <212> PRT  
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<400> 517  
 His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg Glu Cys Arg  
 1 5 10 15

Pro Gln His Cys Cys  
 20

<210> 518  
 <211> 23  
 <212> PRT  
 <213> Conus wittigi

<400> 518  
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 1 5 10 15

Ile Arg His Gln Cys Cys Thr

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<210> 519  
<211> 17  
<212> PRT  
<213> Conus omaria

<400> 519  
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1 5 10 15

Cys

<210> 520  
<211> 17  
<212> PRT  
<213> Conus omaria

<400> 520  
Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly Cys Thr Pro Cys Gly  
1 5 10 15

Cys